



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 184070

TO: Manjunath N Rao
Location: REM-2A01/2C70
Art Unit: 1652
Monday, April 17, 2006
Case Serial Number: 10/784592

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

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STIC-Biotech/ChemLib*184070*

From: Rao, Manjunath N.
Sent: Tuesday, April 04, 2006 9:46 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 10/784592

From: Manjunath N. Rao
Art Unit 1652, **Room** 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 4-4-06

Please search the following as soon as possible for application with serial number
10/784592

1. **SEQ ID NO: 18 and nucleotides 124-744 of SEQ ID NO:18, against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results**
2. **SEQ ID NO: 43 and amino acids 42-248 of SEQ ID NO:43 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.**

If you have any questions please call me at the above phone number.

Thanks

4/4/2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: April 12, 2006, 06:55:51 ; Search time 3612 Seconds
(without alignments)
9772.919 Million cell updates/sec
Title: US-10-784-592-18_COPY_124_744
Perfect score: 621
Sequence: 1 aacacgtgtatgattcg.....aaacgacgtatgcttcttcg 621
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				GenEmbl:*			
				1: gb_ba:*			
				2: gb_in:*			
				3: gb_env:*			
				4: gb_on:*			
				5: gb_ov:*			
				6: gb_pat:*			
				7: gb_ph:*			
				8: gb_pr:*			
				9: gb_ro:*			
				10: gb_sts:*			
				11: gb_sy:*			
				12: gb_un:*			
				13: gb_vi:*			
				14: gb_htg:*			
				15: gb_pi:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description		
1	621	100.0	744	6	CS130878	Sequence	
c	40.8	6.6	110000	1	BA000004	Continuation (32 o	
2	40.2	6.5	239687	14	CR932017	Danio rer	
3	39.8	6.4	200322	14	AC164371	Bos tauru	
4	39.4	6.3	204839	14	AC144882	Gorilla g	
5	39.4	6.3	204839	14	AC144882	Gorilla g	
6	38.6	6.2	110000	2	AC116984_2	Continuation (3 of	
7	38.6	6.2	110000	2	AC116984_3	Continuation (4 of	
c	38.6	6.2	244259	14	AC123226	Rattus no	
8	38.6	6.2	257204	14	AC109987	Rattus no	
9	38.6	6.2	116374	5	BX571959	Zebrafish	
c	38.2	6.2	242081	14	CR933779	Danio rer	
10	38.2	6.2	242081	14	CR933779	Danio rer	
11	37.8	6.1	1554	15	AF225410	Gastrodia	
12	37.8	6.1	173237	14	AY032588	Gastrodia	
c	37.8	6.1	181924	14	AC155611	Zea mays	
13	37.8	6.1	181924	14	AC155611	Zea mays	
14	37.8	6.1	200412	14	AC115666	Rattus no	
15	37.8	6.1	200412	14	AC115666	Rattus no	
c	37.8	6.1	279242	14	AC114079	Rattus no	
16	37.8	6.1	279242	14	AC114079	Rattus no	
17	37.8	6.1	279242	14	AC114079	Rattus no	
18	37.8	6.1	346208	14	AC128290	Rattus no	

c	19	37.4	6.0	2000	6	AX655393	Sequence
	20	37	6.0	39961	8	AC000044	Homo sapi
	21	37	6.0	43738	8	AC000034	Homo sapi
c	22	36.6	5.9	2286	15	LEU78526	Lycopersico
	23	36.4	5.9	176422	9	AC158170	Mus muscu
	24	36.2	5.8	387	15	AF123309	Gastrodia
	25	36.2	5.8	516	15	GEL277784	Gastrodia
	26	36.2	5.8	687	15	GEL277785	Gastrodia
	27	36.2	5.8	687	15	GEL277786	Gastrodia
	28	36.2	5.8	699	15	GEL277783	Gastrodia
	29	36.2	5.8	2306	15	AF334813	Gastrodia
	30	36.2	5.8	110000	15	AP008217	Continuation (238
	31	36.2	5.8	149697	15	AC109832_237	Continuation (238
	32	36.2	5.8	180695	14	AC109832	Oryza sat
	33	36	5.8	63331	14	AC140661	AC109832 Oryza sat
c	34	36	5.8	216589	14	AC084345	AC109832 Oryza sat
c	35	35.6	5.7	26557	8	DQ001128	AC084345 Homo sapi
	36	35.6	5.7	79438	8	HSDJ547C9	AC091741 Homo sapi
	37	35.6	5.7	134953	14	AC026088	DQ001128 Homo sapi
	38	35.6	5.7	154350	8	AC016948	AL109927 Human DNA
	39	35.6	5.7	194418	5	EX001055	AC026088 Homo sapi
c	40	35.6	5.7	197196	14	AC112585	AC016948 Homo sapi
c	41	35.6	5.7	254684	14	AC094805	AC112585 Rattus no
c	42	35.2	5.7	482	15	AF472209	AC094805 Rattus no
c	43	35.2	5.7	482	15	AF472211	AF472209 Arabidops
c	44	35.2	5.7	482	15	AF472212	AF472211 Arabidops
c	45	35.2	5.7	482	15	AF472213	AF472212 Arabidops

ALIGNMENTS

RESULT 1
CS130878
LOCUS CS130878 744 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 18 from Patent WO2005066339.
ACCESSION CS130878
VERSION CS130878.1 GI:71793146
KEYWORDS Alicyclobacillus sp.
SOURCE Alicyclobacillus sp.
ORGANISM Alicyclobacillus sp.
Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
Alicyclobacillus.

REFERENCE 1
AUTHORS Wilting,R.
TITLE Polypeptides of Alicyclobacillus sp
JOURNAL Patent: WO 2005066339-A 18 21-JUL-2005;
Novozymes A/S (DK)
FEATURES
source Location/Qualifiers
1..744
/organism="Alicyclobacillus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:61169"

misc_feature 1..744
/note="CDS"
misc_feature 1..123
/note="sig_peptide"
misc_feature 124..744
/note="mat_peptide"

ORIGIN

Query Match 100.0%; Score 621; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.2e-183;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACACGGTGTATGATTCGAGGAACACACCGCGGACGCATCAAGCGTAAAGCGTACA 60
DB 124 AACACGGTGTATGATTCGAGGAACACACCGCGGACGCATCAAGCGTAAAGCGTACA 183
QY 61 ACTTCTTTGGTTAATTCGACGAATAGTTTCACAGTAGCAAGCAAGCAAACTCCAGT 120
DB 184 ACTTCTTTGGTTAATTCGACGAATAGTTTCACAGTAGCAAGCAAGCAAACTCCAGT 243

```
QY 121 ACGTCTCCGCTCATAGTCTAGAACTCATTTGCAACATGCGCAACATCAAGTGTCTACG 180
Db 244 ACGTCTCCGCTCATAGTCTAGAACTCATTTGCAACATGCGCAACATCAAGTGTCTACG 303
QY 181 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCCGTTTCACACATACGGGAGGTAGGA 240
Db 304 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCCGTTTCACACATACGGGAGGTAGGA 363
QY 241 GACTTGGAAATAGAGTTAACTCCCTGCAGCAAGTTAAAGAGTGTGGGGTACGACGGGATA 300
Db 364 GACTTGGAAATAGAGTTAACTCCCTGCAGCAAGTTAAAGAGTGTGGGGTACGACGGGATA 423
QY 301 GGTGAACCCGAAATGGTGGTGGTTTGGTTTATCAACATCACCATAGAAATGACGGATCC 360
Db 424 GGTGAACCCGAAATGGTGGTGGTTTGGTTTATCAACATCACCATAGAAATGACGGATCC 483
QY 361 ACTCCTATGAGGTCGTTGATGATATTCATTTGCGAAGTAAACGGGAGCGTTTAT 420
Db 484 ACTCCTATGAGGTCGTTGATGATATTCATTTGCGAAGTAAACGGGAGCGTTTAT 543
QY 421 CAGCGGATTTCTACTGCTGAGATATATGCAAAATACAAATTCAGGACTATTCGACCGAC 480
Db 544 CAGCGGATTTCTACTGCTGAGATATATGCAAAATACAAATTCAGGACTATTCGACCGAC 603
QY 481 CTCAACCTGGTGTCCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 540
Db 604 CTCAACCTGGTGTCCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 663
QY 541 TATGGTCACGTCGGGACGATTTACTCATTTGCTTCCATGGTTCCTTCGGGTACAGT 600
Db 664 TATGGTCACGTCGGGACGATTTACTCATTTGCTTCCATGGTTCCTTCGGGTACAGT 723
QY 601 GAAACGACGTATGCTCTTCGG 621
Db 724 GAAACGACGTATGCTCTTCGG 744
```

RESULT 2
BA000004_31/c
WPCOMMENT

Sequence split into 42 fragments LOCUS BA000004 Accession BA000004

Fragment Name	Begin	End
BA000004_00	1	110000
BA000004_01	100001	210000
BA000004_02	200001	310000
BA000004_03	300001	410000
BA000004_04	400001	510000
BA000004_05	500001	610000
BA000004_06	600001	710000
BA000004_07	700001	810000
BA000004_08	800001	910000
BA000004_09	900001	1010000
BA000004_10	1000001	1110000
BA000004_11	1100001	1210000
BA000004_12	1200001	1310000
BA000004_13	1300001	1410000
BA000004_14	1400001	1510000
BA000004_15	1500001	1610000
BA000004_16	1600001	1710000
BA000004_17	1700001	1810000
BA000004_18	1800001	1910000
BA000004_19	1900001	2010000
BA000004_20	2000001	2110000
BA000004_21	2100001	2210000
BA000004_22	2200001	2310000
BA000004_23	2300001	2410000
BA000004_24	2400001	2510000
BA000004_25	2500001	2610000
BA000004_26	2600001	2710000
BA000004_27	2700001	2810000
BA000004_28	2800001	2910000
BA000004_29	2900001	3010000
BA000004_30	3000001	3110000

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BA000004_31 3100001 3210000
BA000004_32 3200001 3310000
BA000004_33 3300001 3410000
BA000004_34 3400001 3510000
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BA000004_36 3600001 3710000
BA000004_37 3700001 3810000
BA000004_38 3800001 3910000
BA000004_39 3900001 4010000
BA000004_40 4000001 4110000
BA000004_41 4100001 4202352
Continuation (32 of 42) of BA000004 from base 3100001 (BA000004 Bacillus halodurans C-12)

Query Match 6.6%; Score 40.8; DB 1; Length 110000;
Best Local Similarity 51.8%; Pred. No. 0.49;
Matches 118; Conservative 0; Mismatches 107; Indels 3; Gaps 1;

QY 303 TGAACCGCAAAATGGTGGTGGTTTGGTTTATCAACATCACCATAGAAATGACGGATCCAC 362
Db 87150 TGCAGAGGCGAAAGGAACTTTCTCTATTGTAGATGTAAACAATCAAAAATGAAGGAGCGA 87091
QY 363 TCCTATGAGGTCGTTGATGCGCATATTCATTTGCGAAGTAAACGGGAGCGTTTATCA 422
Db 87090 CTCTATTACGTTGATTCGTTCTTTTAAATTAAGTCGGAGATG---TAGAATATGA 87034
QY 423 GCCGGATTTCTACTGCTGAGATATATGCAATACAAATTCAGGAGCACTATTCGACCGACCT 482
Db 87033 TTCTGATTCCTCTGCTGGACTTTACGGGATGAAGTGTCTGACTTTTCTCTACTAAGCT 86974
QY 483 CAACCTCGTGTGTCATGACGACAAATCTCGTATTTGATATGCGCGA 530
Db 86973 AAATCCTGGTTTGGAACTACCAGGTAAAGTGTATTTGATGTTTCCGCA 86926
```

RESULT 3
CR932017

DEFINITION CR932017 239687 bp DNA linear HTG 22-MAY-2005
LOCUS Danio rerio clone DKEY-33F9, WORKING DRAFT SEQUENCE, 7 unordered
pieces.

ACCESSION CR932017

VERSION CR932017.4 GI:6392865

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 239687)

AUTHORS McLaren,S.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfsh-help@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk

On May 22, 2005 this sequence version replaced gi:56797647.

COMMENT ----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: zfsh-help@sanger.ac.uk

----- Project Information

Center project name: zK33F9

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 235298 bases at least Q40

Consensus quality: 235832 bases at least Q30

Consensus quality: 236380 bases at least Q20

Insert size: 239087; sum-of-contigs

Insert size: 217257; 9.8% error; agarose-fp

Quality coverage: 9.53x in Q20 bases; sum-of-contigs Quality

coverage: 10.66x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: FHSB

Center clone name: CH240-11714

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 190643 bases at least Q40

Consensus quality: 193630 bases at least Q30

Consensus quality: 195478 bases at least Q20

Estimated insert size: 198954; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 5877: contig of 5877 bp in length
* 5878 6322: gap of 445 bp
* 6323 18172: contig of 11850 bp in length
* 18173 18222: gap of 50 bp
* 18223 20526: contig of 2304 bp in length
* 20527 20576: gap of 50 bp
* 20577 35742: contig of 15166 bp in length
* 35743 36222: gap of 480 bp
* 36223 38281: contig of 2059 bp in length
* 38282 38381: gap of unknown length
* 38382 41147: contig of 2766 bp in length
* 41148 41197: gap of 50 bp
* 41198 55437: contig of 14240 bp in length
* 55438 55562: gap of 125 bp
* 55563 86280: contig of 30718 bp in length
* 86281 86330: gap of 50 bp
* 86331 92028: contig of 5698 bp in length
* 92029 92078: gap of 50 bp
* 92079 119970: contig of 27892 bp in length
* 119971 120047: gap of 77 bp
* 120048 123376: contig of 3328 bp in length
* 123376 123665: gap of 290 bp
* 123666 142980: contig of 19315 bp in length
* 142981 143080: gap of unknown length
* 143081 144260: contig of 1180 bp in length
* 144261 145079: gap of 819 bp
* 145080 192359: contig of 47280 bp in length
* 192360 192459: gap of unknown length
* 192460 193549: contig of 1090 bp in length
* 193550 193649: gap of unknown length
* 193650 195025: contig of 1376 bp in length
* 195026 195125: gap of unknown length
* 195126 196204: contig of 1079 bp in length
* 196205 196304: gap of unknown length
* 196305 197805: contig of 1501 bp in length
* 197806 197905: gap of unknown length
* 197906 200322: contig of 2417 bp in length.

FEATURES

source

Location/Qualifiers
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-11714"
5878. .6322
/estimated_length=445
18173. .18222
/estimated_length=50
20527. .20576
/estimated_length=50
35743. .36222
/estimated_length=480
38282. .38381
/estimated_length=unknown
41148. .41197
/estimated_length=50
55438. .55562
/estimated_length=125
86281. .86330
/estimated_length=50
92029. .92078
/estimated_length=50
119971. .120047
/estimated_length=77
123376. .123665
/estimated_length=290
142981. .143080
/estimated_length=unknown
144261. .145079
/estimated_length=819
192360. .192459
/estimated_length=unknown
193550. .193649
/estimated_length=unknown
195026. .195125
/estimated_length=unknown
196205. .196304
/estimated_length=unknown
197806. .197905
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Query Match 6.4%; Score 39.8; DB 14; Length 200322;

Best Local Similarity 60.7%; Pred.No.1;

Matches 65; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 199 AAGTTACGATATATCCCGTTTCACATACGGAAGTAGGAGACTTTGGAAATTAGAGTT 258

Db 13752 AGGTGAGCACATGGCACAGTCTTCTCTCCGGAAGTAGGAGACTCTCTGGAGATTAGAGGA 13811

Qy 259 AACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATAGGTGA 305

Db 13812 AAAACCCCTCTGATAGATACAAATCTGGGCTCTCGGGGAAAGGGGA 13858

RESULT 5

AC144882

LOCUS

DEFINITION

AC144882 204839 bp DNA linear HTG 18-JUN-2003

2 ordered pieces.

AC144882

AC144882.2 GI:31880084

HTG; HTGS PHASE2; HTGS DRAFT.

KEYWORDS

SOURCE

ORGANISM

Gorilla gorilla gorilla (lowland gorilla)

Gorilla gorilla gorilla

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Gorilla

1 (bases 1 to 204839)

ANTHROPUS

Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K.,

Beckstrom-Sternberg,S.M., Benjamin,B.,

Antoneilis,A., Ayele,K., Brinkley,C., Brooks,S., Cariaga,K.,

Beckstrom-Sternberg,S.M., Benjamin,B.,

Antoneilis,A., Ayele,K., Brinkley,C., Brooks,S., Cariaga,K.,

Beckstrom-Sternberg,S.M., Benjamin,B.,

Antoneilis,A., Ayele,K., Brinkley,C., Brooks,S., Cariaga,K.,

Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurie, B., Idoi, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.B., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 204839)
 Green, E.D.
 Direct Submission
 Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 3 (bases 1 to 204839)
 Green, E.D.
 Direct Submission
 Submitted (18-JUN-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 On Jun 18, 2003 this sequence version replaced gi:31044297.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc.zoemhgr@nih.gov
 ----- Project Information
 Center project name: enf
 Center clone name: 154N17

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 204590 bases at least Q40
 Consensus quality: 204680 bases at least Q30
 Consensus quality: 204709 bases at least Q20
 Insert size: 192000; agarose-fp
 Insert size: 204739; sum-of-contigs
 Quality coverage: 11.99x in Q20 bases; agarose-fp
 Quality coverage: 11.24x in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 187431: contig of 187431 bp in length
 * 187432 187531: gap of unknown length
 * 187532 204839: contig of 17308 bp in length.

FEATURES

Location/Qualifiers
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 /mol_type="genomic DNA"
 /sub_species="gorilla"
 /db_xref="taxon:9595"
 /clone="CH255-154N17"

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/clone_lib="CH255"
1..187431
/note="assembly_fragment
clone_end:T7
vector_side:left"
1..15517
/note="clone overlaps with GenBank Accession Number
AC144464 clone CH255-473J23 (center project name enf)"
187432..187531
/estimated_length=unknown
187532..204839
/note="assembly_fragment
clone_end:SP6
vector_side:right"

ORIGIN
Query Match      6.3%; Score 39.4; DB 14; Length 204839;
Best Local Similarity 52.1%; Pred. No. 1.4;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 259 AACTCCCTGCGAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAACCGCAAAATGGT 318
Db      |||||
Qy 319 GCGTTTTGGGTTATCAACATCACCATGAAGAATGACGGATCCACTCCTATGAGGTGCTT 378
Db      |||||
Qy 69409 GCCTATAGCCTTAGCCACAGCAACATATAAATGTTAAATCTAACCTTAATGCAGGGCTTG 69468
Db      |||||
Qy 379 GATGGCATATTCCATTTTCAGAACTTAAACGGGAACGTTTATCAGCCGG 427
Db      |||||
Qy 69469 CTTCTGCCACCTGATTTTAGAAATATAGTGTATATTTCTTCCCTGG 69517
Db      |||||

RESULT 6
AC116984_2
WPCOMMENT
Sequence split into 6 fragments LOCUS AC116984 Accession AC116984
Fragment Name      Begin      End
AC116984_0         1      110000
AC116984_1        100001    210000
AC116984_2        200001    310000
AC116984_3        300001    410000
AC116984_4        400001    510000
AC116984_5        500001    541399
Continuation (3 of 6) of AC116984 from base 200001 (AC116984 Dictyostelium discoideum ch

Query Match      6.2%; Score 38.6; DB 2; Length 110000;
Best Local Similarity 51.4%; Pred. No. 2.4;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGTGAAACCGCAAAATGGTGCCTTTTGGGTTATCAACATCACCATAAGAAATGACGGAT 358
Db      |||||
Qy 100885 TGGTTGAAAAGAAAATAAAAAAGTTAATGATTAATCAACAAAACCGTATTAGATGTCGAAT 100944
Db      |||||
Qy 359 CCATCTCTATGGAGGTGTTGATGCGATATTCCTATTCGAGAACTTAACCGGACGTTT 418
Db      |||||
Qy 100945 CTTTGTGTAATGATCACCACGGTGGTTAGCTTACATTAATAATGGGTATTGCTGAAGATG 101004
Db      |||||
Qy 419 ATCAGCCGGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
Db      |||||
Qy 101005 CAATTCATGTTTACTGTTGAGTATTATGCTCAATCAATGCTGCTAAAAAT 101057
Db      |||||

RESULT 7
AC116984_3
WPCOMMENT
Sequence split into 6 fragments LOCUS AC116984 Accession AC116984
Fragment Name      Begin      End
AC116984_0         1      110000
AC116984_1        100001    210000
AC116984_2        200001    310000
AC116984_3        300001    410000
AC116984_4        400001    510000

```

Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
Williams, G., Willison, R., Wluczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederstock, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 244259)
Worley, K.C.
Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 244259)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21671648.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSVF
Center clone name: CH230-217M18
----- Summary Statistics
Assembly program: Phrap; version 0.930239
Consensus quality: 174893 bases at least Q40
Consensus quality: 180721 bases at least Q30
Consensus quality: 184098 bases at least Q20
Estimated insert size: 195426; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 131499: contig of 131499 bp in length
* 131500 131599: gap of unknown length
* 131600 231486: contig of 99887 bp in length
* 231487 231586: gap of unknown length
* 231587 232741: contig of 1155 bp in length
* 232742 232841: gap of unknown length
* 232842 234462: contig of 1621 bp in length
* 234463 234562: gap of unknown length
* 234563 236227: contig of 1665 bp in length
* 236228 236327: gap of unknown length

FEATURES		Location/Qualifiers	
+	236328	237975: contig of 1648 bp in length	
*	237976	238075: gap of unknown length	
*	238076	241664: contig of 3589 bp in length	
*	241665	241764: gap of unknown length	
*	241765	244259: contig of 2495 bp in length.	
source		1. .244259	
		/organism="Rattus norvegicus"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:10116"	
		/clone="CH230-217M18"	
misc_feature		1. .1078	
		/note="wgs contig"	
misc_feature		33392. .34674	
		/note="wgs contig"	
misc_feature		81130. .82304	
		/note="wgs contig"	
misc_feature		93183. .94437	
		/note="wgs contig"	
gap		131500. .131599	
		/estimated_length=unknown	
misc_feature		199589. .201827	
		/note="wgs contig"	
gap		231487. .231586	
		/estimated_length=unknown	
gap		232742. .232841	
		/estimated_length=unknown	
gap		234463. .234562	
		/estimated_length=unknown	
gap		236228. .236327	
		/estimated_length=unknown	
gap		237976. .238075	
		/estimated_length=unknown	
gap		241665. .241764	
		/estimated_length=unknown	
ORIGIN			
Query Match 6.2%; Score 38.6; DB 14; Length 244259;			
Best Local Similarity 54.6%; Pred. NO. 2.5;			
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;			
QY	381	TGCGCATATTCATTTCGACGAACTTAACGGGAACGTTTATCATCGCGGATCTTACTGCTGA	440
Db	96563	TGCGCATCTTGGAAATTCGAGCCCTTATATGTAAGAGGTAGCCATCTGAACCTTACTCCTTA	96504
QY	441	GATATATGCAATACAAATTCAGGGACTATTCGACCGACCTCAACCCCTGGTGTCAT	500
Db	96503	CATTTTCCGAGAGGCCATTCATACACTGAGCCATCACCACACCCCATATGTGTTAAT	96444
QY	501	GACGACAAATCTCGTATTGA	521
Db	96443	AGTTCTAAGACCTACATTGA	96423
RESULT 9			
AC109987			
LOCUS	Rattus norvegicus clone CH230-230B23, *** SEQUENCING IN PROGRESS		
DEFINITION	AC109987 257204 bp DNA linear HTG 11-OCT-2002		
	***, 13 unordered pieces.		
ACCSSTON	AC109987		
VERSION	AC109987.4 GI:23820637		
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Rattus.		
AUTHORS	1 (bases 1 to 257204) Muzny, D. Marie, Metzker, M. Lee, Abranzen, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyatebechi, V., Ayoyaj, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Muzny, D. Marie, Metzker, M. Lee, Abranzen, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyatebechi, V., Ayoyaj, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.		

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregregories, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huiyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, J., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorusshewe, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okwuonu, G., Olarnpungsoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puzos, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Stealmie, M., Strong, R., Sutton, A., Svatek, A., Tabori, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wleczkyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederstock, G., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 257204)
Worley K.C.
Direct Submission
Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 257204)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2002 this sequence version replaced gi:21739166.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine

----- Genome Center
Center: Baylor College of Medicine

```

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRIS
Center clone name: CH230-230B23
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 231067 bases at least Q40
Consensus quality: 235027 bases at least Q30
Consensus quality: 237586 bases at least Q20
Estimated insert size: 229826; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* [see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html].
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 2601: contig of 2601 bp in length
* 2602
* 2701: gap of unknown length
* 2702
* 232156: contig of 229455 bp in length
* 232157
* 232256: gap of unknown length
* 232257
* 241482: contig of 9226 bp in length
* 241483
* 241582: gap of unknown length
* 241583
* 242756: contig of 1173 bp in length
* 242757
* 242855: gap of unknown length
* 242856
* 243963: contig of 1108 bp in length
* 243964
* 244063: gap of unknown length
* 244064
* 245276: contig of 1213 bp in length
* 245277
* 245376: gap of unknown length
* 245377
* 246513: contig of 1137 bp in length
* 246514
* 246613: gap of unknown length
* 246614
* 248232: contig of 1619 bp in length
* 248233
* 248332: gap of unknown length
* 248333
* 249982: contig of 1650 bp in length
* 249983
* 250082: gap of unknown length
* 250083
* 252270: contig of 2188 bp in length
* 252271
* 252370: gap of unknown length
* 252371
* 253471: contig of 1101 bp in length
* 253472
* 253571: gap of unknown length
* 253572
* 255719: contig of 2148 bp in length
* 255720
* 255819: gap of unknown length
* 255820
* 257204: contig of 1385 bp in length.
*
* Location/Qualifiers
* 1..257204
*   /organism="Rattus norvegicus"
*   /mol_type="genomic DNA"
*   /db_xref="taxon:10116"
*   /clone="CH230-230B23"
*
* 1..1057
*   /note="wgs_end_extension
*   clone_end:Sp6"
*   2602..2701
*   /estimated_length=unknown
*   /note="wgs_end_extension
*   clone_end:Sp6"
*   2702..3930
*   /note="wgs_end_extension
*   clone_end:Sp6"
*   3251..3632
*   /note="clone_boundary
*   clone_end:Sp6
*   site:ECORI
*   end_sequence:RWB0G12TV"
* 220094..220968
*   /note="clone_boundary
*   clone_end:T7
*   site:ECORI
*   end_sequence:RWB0G12TJ"

```

```

misc_feature 230983..232156
              /note="wgs_end_extension
              clone_end:T7"
gap          232157..232256
              /estimated_length=unknown
gap          241483..241582
              /estimated_length=unknown
gap          242756..242855
              /estimated_length=unknown
gap          243964..244063
              /estimated_length=unknown
gap          245277..245376
              /estimated_length=unknown
gap          246514..246613
              /estimated_length=unknown
gap          248233..248332
              /estimated_length=unknown
gap          249983..250082
              /estimated_length=unknown
gap          252271..252370
              /estimated_length=unknown
gap          253472..253571
              /estimated_length=unknown
gap          255720..255819
              /estimated_length=unknown
ORIGIN
Query Match      6.2%; Score 38.6; DB 14; Length 257204;
Best Local Similarity 54.6%; Pred. No. 2.5;
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 381 TGCATATTCATTTCAGAACTTAAACGGGAACGTTTATCAGCCGGAATCTACTGCTGA 440
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28833 TGGCATTCGGAATTCGAGCCCTTATATGTAAGGGTAGCCATCTGAACCTCTACTCTTA 28892
Qy 441 GATATATGCAATACAAATTCAGGAGCTATTCGACCGCACTCAACCCCTGGTGTCCAT 500
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28893 CATTTTTCCAGAGGCCATTCATACACTGAGCCATCACCCCAACACCATATGTGTTAAT 28952
Qy 501 GACGACAAATCTCGTATTGGA 521
      |||||
Db 28953 AGTTCTAAGACCTACATTGGA 28973

RESULT 10
BX571959/c 116374 bp DNA linear VRT 05-NOV-2004
LOCUS Zebrafish DNA sequence from clone DKEY-4616 in linkage group 12,
DEFINITION complete sequence.
ACCESSION BX571959 GI:55467255
VERSION BX571959.8
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
          Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 116374)
AUTHORS Barker, D.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 5, 2004 this sequence version replaced gi:54304257.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

```

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see

http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-4616 is from a Zebrafish BAC library

VECTOR: pindigobac-5.

FEATURES

```

source
1. .116374
   Location/Qualifiers
   /organism="Danio rerio"
   /mol_type="genomic DNA"
   /db_xref="taxon:7955"
   /clone="DKEY-4616"
   /clone_lib="DanioKey"

```

ORIGIN

```

Query Match      6.2%  Score 38.2;  DB 5;  Length 116374;
Best Local Similarity 59.8%;  Pred. No. 3.2;
Matches 64;  Conservative 0;  Mismatches 43;  Indels 0;  Gaps 0;

```

```

QY 385 ATATTCATTGACAGACTTAAACGGAACTTTATCAGCGGAGTTCTACTGCTGAGATA 444
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47200 ATATTCAAATTAGTTCTTAGCAGGAAATTTACTAACAGATATTAAGTTTGATATA 47141
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 445 TATGCAATCAAAATTCAGGACTATTCGACGACCTCAACCTCG 491
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47140 TTTCTGTAGAAATTCACAGATATTTTCATAGAACTCAACCTTG 47094
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 11

CR933779/c

LOCUS

CR933779 242081 bp DNA linear HTG 10-JUN-2005
 Danio rerio chromosome 12 clone DKEY-13J5, WORKING DRAFT SEQUENCE,
 12 unordered pieces.

ACCESSION

CR933779

VERSION

CR933779.4 GI:67509338

KEYWORDS

HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.

SOURCE

Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 242081)

McLaren.S.

Direct Submission

Submitted (08-JUN-2005) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests:

http://www.sanger.ac.uk/Projects/D_rerio/faqs.shtml#dataeight

On Jun 10, 2005 this sequence version replaced gi:58330714.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

----- Project Information

Center project name: zk13J5

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 236648 bases at least Q40

Consensus quality: 237713 bases at least Q30

Consensus quality: 238743 bases at least Q20

Insert size: 240981; sum-of-contigs

Insert size: 168181; 37.4% error; agarose-fp

Quality coverage: 6.79x in Q20 bases; sum-of-contigs Quality

coverage: 9.84x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

* 1
* 3578: contig of 3578 bp in length
* 3579
* 3678: gap of 100 bp
* 3679
* 13686: contig of 10008 bp in length
* 13687
* 13786: gap of 100 bp
* 13787
* 45507: contig of 31721 bp in length
* 45508
* 45607: gap of 100 bp
* 45608
* 60434: contig of 14827 bp in length
* 60435
* 60534: gap of 100 bp
* 60535
* 72346: contig of 11812 bp in length
* 72347
* 72446: gap of 100 bp
* 72447
* 79048: contig of 6602 bp in length
* 79049
* 79148: gap of 100 bp
* 79149
* 90278: contig of 11130 bp in length
* 90279
* 90378: gap of 100 bp
* 90379
* 131546: contig of 41168 bp in length
* 131547
* 131646: gap of 100 bp
* 131647
* 141611: contig of 9965 bp in length
* 141612
* 141711: gap of 100 bp
* 141712
* 173884: contig of 32173 bp in length
* 173885
* 173984: gap of 100 bp
* 173985
* 237730: contig of 63746 bp in length
* 237731
* 237830: gap of 100 bp
* 237831
* 242081: contig of 4251 bp in length.

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FEATURES

source

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1. .242081
   /organism="Danio rerio"
   /mol_type="genomic DNA"
   /db_xref="taxon:7955"
   /chromosome="12"
   /clone="DKEY-13J5"
   /clone_lib="DanioKey"

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misc_feature

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1. .3578
   /note="assembly fragment:01599"
   fragment_chain:1
   3679..13686
   /note="assembly fragment:01661"
   fragment_chain:1

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misc_feature

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13787..45507
   /note="assembly fragment:02271"
   fragment_chain:1
   45608..60434
   /note="assembly fragment:02110"
   fragment_chain:1

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misc_feature

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60535..72346
   /note="assembly fragment:01984"
   fragment_chain:1
   72447..79048
   /note="assembly fragment:01793"
   fragment_chain:1

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misc_feature

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79149..90278

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RESULT 14
AC155465/c

LOCUS

DEFINITION AC155465 173237 bp DNA linear HTG 25-JAN-2005
Zea mays strain B73 clone ZWMBB0518K03, *** SEQUENCING IN PROGRESS
*** 20 unordered pieces.

ACCESSION

AC155465
AC155465.2 GI:58082326

KEYWORDS

HTG; HTGS_PHASE1.

SOURCE

Zea mays
Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 173237)

AUTHORS

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.

TITLE

Consortium for Maize Genomics - BAC skim sequencing and assembly

REFERENCE

Unpublished
2 (bases 1 to 173237)

AUTHORS

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.

TITLE

Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),

JOURNAL

9712 Medical Center Dr, Rockville, MD 20850

REFERENCE

3 (bases 1 to 173237)

AUTHORS

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.

TITLE

Direct Submission

JOURNAL

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850

COMMENT

On Jan 25, 2005 this sequence version replaced gi:57862986.

----- trace submission

Center name: TIGR

Seq lib id: ZGBD

----- Project information

Web site: <http://www.tigr.org/tdb/tgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2078: contig of 2078 bp in length
* 2079 2178: gap of unknown length
* 2179 4331: contig of 2153 bp in length
* 4332 4431: gap of unknown length
* 4432 7508: contig of 3077 bp in length
* 7509 7609: gap of unknown length
* 7609 9827: contig of 2219 bp in length
* 9828 9928: gap of unknown length
* 9928 12391: contig of 2464 bp in length
* 12392 12491: gap of unknown length
* 12492 20946: contig of 8455 bp in length
* 20947 21046: gap of unknown length
* 21047 25323: contig of 4277 bp in length
* 25324 25423: gap of unknown length
* 25424 58810: contig of 33387 bp in length
* 58811 58910: gap of unknown length

ORIGIN

Query Match 6.1%; Score 37.8; DB 14; Length 173237;

Best Local Similarity 53.8%; Pred. No. 4.3;

Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

* 58911 74261: contig of 15351 bp in length
* 74262 74361: gap of unknown length
* 74362 87576: contig of 13215 bp in length
* 87577 87676: gap of unknown length
* 87677 89714: contig of 2038 bp in length
* 89715 91854: gap of unknown length
* 91855 91954: gap of unknown length
* 91955 95702: contig of 3748 bp in length
* 95703 95802: gap of unknown length
* 95803 98408: contig of 2606 bp in length
* 98409 98508: gap of unknown length
* 98509 100761: contig of 2253 bp in length
* 100762 100861: gap of unknown length
* 100862 103611: contig of 2750 bp in length
* 103612 103711: gap of unknown length
* 103712 126807: contig of 23096 bp in length
* 126808 126907: gap of unknown length
* 126908 130568: contig of 3661 bp in length
* 130569 130668: gap of unknown length
* 130669 170988: contig of 40220 bp in length
* 170989 170988: gap of unknown length
* 170989 173237: contig of 2249 bp in length.

FEATURES
Location/Qualifiers
1..173237
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZWMBB0518K03"
2079..2178
/estimated_length=unknown
4332..4431
/estimated_length=unknown
7509..7608
/estimated_length=unknown
9828..9927
/estimated_length=unknown
12392..12491
/estimated_length=unknown
20947..21046
/estimated_length=unknown
25324..25423
/estimated_length=unknown
58811..58910
/estimated_length=unknown
74262..74361
/estimated_length=unknown
87577..87676
/estimated_length=unknown
89715..89814
/estimated_length=unknown
91855..91954
/estimated_length=unknown
95703..95802
/estimated_length=unknown
98409..98508
/estimated_length=unknown
100762..100861
/estimated_length=unknown
103612..103711
/estimated_length=unknown
126808..126907
/estimated_length=unknown
130569..130668
/estimated_length=unknown
170989..170988
/estimated_length=unknown

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 06:54:15 ; Search time 491 Seconds
(without alignment)
8429.275 Million cell updates/sec

Title: US-10-784-592-18_COPY_124_744

Perfect score: 621

Sequence: 1 aacacgtgtatgatctgc.....aaacgacgtatgctcttcgcg 621

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	100.0	621	14 AEB45582	Aeb45582 Alicyclob
2	621	100.0	744	14 AEB45544	Aeb45544 Alicyclob
3	621	100.0	744	14 AEB48730	Aeb48730 Alicyclob
c 4	37.4	6.0	2000	8 ADA71938	Ada71938 Rice gene
5	36.2	5.8	2306	8 ACC47595	Acc47595 Gastrodia
6	35.6	5.7	7636	5 ABA17217	Abal17217 Human ner
c 7	35.2	5.7	580	10 ADK56798	Adk56798 Plant DNA
8	35	5.6	2349	13 ADS61627	Ads61627 Bacterial
9	35	5.6	42488	4 AAK66772	Aak66772 Human imm
10	34	5.5	2000	11 ACL37108	Ac137108 Rice stre
11	33.8	5.4	729	13 ADX12170	Adx12170 Plant ful
12	33.8	5.4	860	13 ADX12259	Adx12259 Plant ful
c 13	33.4	5.4	706	10 ADK56319	Adk56319 Plant DNA
14	33.2	5.3	2000	8 ADA71938	Ada71938 Rice gene
c 15	33.2	5.3	7480	13 ADP25286	Adp25286 PRO polyp
c 16	33.2	5.3	7480	13 ADY17856	Ady17856 DNA encod
c 17	32.6	5.2	2700	5 AAD14385	Aad14385 Mouse bon
c 18	32.4	5.2	813	8 AAC28717	Aac28717 Prokaryot
c 19	32.4	5.2	18595	4 AAS33411	Aas33411 DNA encod

c 20	32.4	5.2	49999	2 AAZ23899	Aaz23899 Human LOB
21	32.4	5.2	301477	13 ABD33362	Abd33362 Human can
c 22	32.2	5.2	123526	10 ADJ79962	Adj79962 Human gli
23	32	5.2	26147	4 ABL11324	Ab11324 Drosophil
c 24	31.8	5.1	534	6 ABQ55323	Abq55323 Human ova
c 25	31.8	5.1	83432	14 AEA61124	Adk58633 Plant DNA
c 26	31.8	5.1	110000	14 ADZ45062	Adk58633 Plant DNA
c 27	31.6	5.1	704	10 ADK58633	Adk58633 Plant DNA
c 28	31.6	5.1	1007	10 ADK56823	Adk56823 Plant DNA
29	31.6	5.1	2000	11 ACL35887	Adk5887 Rice stre
30	31.6	5.1	110000	10 ACF67367	Adk5887 Rice stre
31	31.6	5.1	110000	10 ACF67367	Adk5887 Rice stre
32	31.6	5.1	110000	10 ACF65387	Adk5887 Rice stre
c 33	31.4	5.1	1412	13 ADR65009	Adk5887 Rice stre
34	31.4	5.1	1572	3 AAZ53068	Aaz53068 Neisseria
35	31.4	5.1	1848	10 ABZ38315	Abz38315 N. gonorr
36	31.4	5.1	1851	3 AAZ53069	Aaz53069 Neisseria
37	31.4	5.1	3531	12 ADQ63920	Adq63920 Novel hum
38	31.4	5.1	9547	6 ABL33505	Ab133505 Human imm
c 39	31.4	5.1	12077	3 AAA81734	Aaa81734 N. mening
c 40	31.4	5.1	17000	6 AAL40299	Aal40299 Caspase 6
41	31.4	5.1	110000	3 AAA81489	Aaa81489 Caspase 6
42	31.4	5.1	349980	3 AAF21612	Aaf21612 Neisseria
43	31.2	5.0	1173	12 ADJ34811	Adj34811 DNA encod
c 44	31.2	5.0	6070	6 ABL33678	Ab133678 Human imm
c 45	31.2	5.0	6070	6 ABL34578	Ab134578 Human met

ALIGNMENTS

RESULT 1

ID AEB45582 standard; DNA; 621 BP.

AC AEB45582;

DT 22-SEP-2005 (first entry)

DE Alicyclobacillus sp. mature functional polypeptide DNA (bases 124-744).

KW Feedstuff; food; detergent; surfactant; pulp; functional polypeptide; gene; ds.

OS Alicyclobacillus sp.; DSM 15716.

FH Key Location/Qualifiers

CDS 1..621

FT /*tag= a

FT /product= "Alicyclobacillus sp. mature functional

FT /polypeptide"

FT /partial

FT /note= "No start and stop codons"

XX US2005147983-A1.

XX 07-JUL-2005.

XX 23-FEB-2004; 2004US-00784592.

XX 06-JAN-2004; 2004DK-00000010.

XX 04-FEB-2004; 2004DK-00000165.

XX (NOVO) NOVOZYMES AS.

XX Wilting R, Lassen SP, Ostergaard PR;

XX WPI; 2005-511773/52.

XX P-PSDB; AEB45583.

XX New functional polypeptides having function and amino acid sequence similar to known specific bacterial enzymes useful in industrial, research and household applications e.g. detergents and food.

```
XX PS Claim 36; Page; 83pp; English.
XX CC The present invention relates to functional polypeptides encoded by
XX CC polynucleotides comprised in the genome of Alicyclobacillus sp. DSM
XX CC 15716. The invention is useful in industrial, research and household
XX CC processes such as in composition to prepare feed and food, in detergent
XX CC formulations and for treating lignocellulosic fabric and pulp. The
XX CC present sequence is Alicyclobacillus sp. DSM 15716 mature functional
XX CC polypeptide DNA. Note: This sequence is not shown in the specification
XX CC but is constructed based on the nucleotide positions provided in claim 36
XX CC of the specification.
XX SQ Sequence 621 BP; 177 A; 142 C; 143 G; 159 T; 0 U; 0 Other;

Query Match      100.0%; Score 621; DB 14; Length 744;
Best Local Similarity 100.0%; Pred. No. 4.6e-195;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGGTGATATGATTTCGAGGAACACACACCGCGGAACGCATCAACGGTAAGCGCTACA 60
Db 1 AACACGGTGATATGATTTCGAGGAACACACACCGCGGAACGCATCAACGGTAAGCGCTACA 60

Qy 61 ACTTCTTTGGTTAATTTCGACGAATAGTTTCACAGTAGCAAAAGCAAGCAAAATCCGAGT 120
Db 61 ACTTCTTTGGTTAATTTCGACGAATAGTTTCACAGTAGCAAAAGCAAGCAAAATCCGAGT 120

Qy 121 ACGTCTCCCGCTCATAGTCTACGAACTCATATTGCAACATGCGCAACATCAAGTGTCTACG 180
Db 121 ACGTCTCCCGCTCATAGTCTACGAACTCATATTGCAACATGCGCAACATCAAGTGTCTACG 180

Qy 181 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 240
Db 181 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 240

Qy 241 GACTTGGAAATTAGATTAACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATA 300
Db 241 GACTTGGAAATTAGATTAACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATA 300

Qy 301 GGTGAAACCGCAATGTGGTGTGGTTTATCAACATCAACATCAACATCAACATCAACATCA 360
Db 301 GGTGAAACCGCAATGTGGTGTGGTTTATCAACATCAACATCAACATCAACATCAACATCA 360

Qy 361 ACTCCTATGAGGTCGTTGATGTCATATTCATTTGCAGAACATTAACGGGAAGCTTTAT 420
Db 361 ACTCCTATGAGGTCGTTGATGTCATATTCATTTGCAGAACATTAACGGGAAGCTTTAT 420

Qy 421 CAGCGGATTTCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTTCCGACCGAC 480
Db 421 CAGCGGATTTCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTTCCGACCGAC 480

Qy 481 CTCAACCTCGTGTGTCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 540
Db 481 CTCAACCTCGTGTGTCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 540

Qy 541 TATGGTCACGTCGCGGACGATTACTCATCTTGTCCGTTCCATGGGTTTCTCGGTCAGAT 600
Db 541 TATGGTCACGTCGCGGACGATTACTCATCTTGTCCGTTCCATGGGTTTCTCGGTCAGAT 600

Qy 601 GAAACGACGTATGCTCTTCCG 621
Db 601 GAAACGACGTATGCTCTTCCG 621

RESULT 2
AEB45544
ID AEB45544 standard; DNA; 744 BP.
XX AC AEB45544;
XX DT 22-SEP-2005 (first entry)
XX DE Alicyclobacillus sp. functional polypeptide DNA, SEQ ID NO: 18.

XX KW Feedstuff; food; detergent; surfactant; pulp; functional polypeptide;
XX KW gene; ds.
XX OS Alicyclobacillus sp.; DSM 15716.
XX PH Key Location/Qualifiers
XX CDS 1..744
FT /tag= b
FT /product= "Alicyclobacillus sp. functional polypeptide"
FT /transl_except= (pos:1..3, aa:Met)
FT /partial
FT /note= "No start and stop codons"
FT sig_peptide 1..123
FT /tag= a
FT mat_peptide 124..744
FT /tag= c
FT /product= "Alicyclobacillus sp. mature functional
FT polypeptide"
XX US2005147983-A1.
XX 07-JUL-2005.
XX 23-FEB-2004; 2004US-00784592.
XX 06-JAN-2004; 2004DK-00000010.
XX 04-FEB-2004; 2004DK-00000165.
XX (NOVO ) NOVOZYMES AS.
XX Wilting R, Lassen SF, Oestergaard PR;
XX WPI; 2005-511773/52.
XX P-PSDB; AEB45569.
XX New functional polypeptides having function and amino acid sequence
XX similar to known specific bacterial enzymes useful in industrial,
XX research and household applications e.g. detergents and food.
XX Example 3; SEQ ID NO 18; 83pp; English.
XX The present invention relates to functional polypeptides encoded by
XX CC polynucleotides comprised in the genome of Alicyclobacillus sp. DSM
XX CC 15716. The invention is useful in industrial, research and household
XX CC processes such as in composition to prepare feed and food, in detergent
XX CC formulations and for treating lignocellulosic fabric and pulp. The
XX CC present sequence is Alicyclobacillus sp. DSM 15716 functional polypeptide
XX CC DNA.
XX SQ Sequence 744 BP; 202 A; 159 C; 179 G; 204 T; 0 U; 0 Other;

Query Match      100.0%; Score 621; DB 14; Length 744;
Best Local Similarity 100.0%; Pred. No. 5e-195;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGGTGATATGATTTCGAGGAACACACACCGCGGAACGCATCAACGGTAAGCGCTACA 60
Db 124 AACACGGTGATATGATTTCGAGGAACACACACCGCGGAACGCATCAACGGTAAGCGCTACA 183

Qy 61 ACTTCTTTGGTTAATTTCGACGAATAGTTTCACAGTAGCAAAAGCAAGCAAAATCCGAGT 120
Db 184 ACTTCTTTGGTTAATTTCGACGAATAGTTTCACAGTAGCAAAAGCAAGCAAAATCCGAGT 243

Qy 121 ACGTCTCCCGCTCATAGTCTACGAACTCATATTGCAACATGCGCAACATCAAGTGTCTACG 180
Db 244 ACGTCTCCCGCTCATAGTCTACGAACTCATATTGCAACATGCGCAACATCAAGTGTCTACG 303

Qy 181 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 240
Db 304 ACTTCATCTTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 363

Qy 241 GACTTGGAAATTAGATTAACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATA 300
```


XX Claim 1; Page 7-8 (Disclosure); 1lpp; Chinese.
PS The invention relates to a fungus-inducible promoter from the plant
XX *Gastrodia elata*. The promoter is that of the *Gastrodia* antifungal protein
CC (GAPP) gene which is expressed in the tubers of the plant. The fungus-
CC inducible promoter may be used in transgenic plants to mediate expression
CC of heterologous genes in the presence of fungus. The present sequence
CC represents the GAPP gene sequence which includes its promoter
XX
SQ Sequence 2306 BP; 735 A; 416 C; 441 G; 714 T; 0 U; 0 Other;

Query Match 5.8%; Score 36.2; DB 8; Length 2306;
Best Local Similarity 57.5%; Pred. No. 0.89;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 256 GTTAACCTCCCTGACGAGTTAAGAGTGTGGGTACGACGGGATAGTGAACCGCAAT 315
Db 1631 GGTAACCTACTATCTGATCCCTTCAGAGAGATCGTAACGTCGTATACGATAATCTCAAT 1690

Qy 316 GGTGCGTTTGGTGTATCAACATCACCATAGAAATGACGGATCCACTCTTAT 368
Db 1691 AATCGATTTGGCAACCCACCAACCGTTGGAATGCTGAATCACTGTCTAT 1743

RESULT 6
ABAI7217
ID ABAI7217 standard; DNA; 7636 BP.
AC ABAI7217;
XX
DT 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 9548.
DE
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
KW antineumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX WO200159063-A2.
PN
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209457P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 25-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 26-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0242221P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 03-DEC-2000; 2000US-0250391P.
PR 03-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system cancers
XX and metastases.
XX
XX Disclosure; SEQ ID NO 9548; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABR11004-ABR21534) and proteins
XX (ABR14678-ABR18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischaemias; (d) wound healing
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 7636 BP; 2263 A; 1773 C; 1517 G; 2083 T; 0 U; 0 Other;

Query Match 5.7%; Score 35.6; DB 5; Length 7636;
Best Local Similarity 54.6%; Pred. No. 2.4;
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 86 GTTCACAGGTAGCAAGCAAGCAAACTCGAGTAGCTCTCCCGCTCATAAGTCTACGA 145
Db 2982 GTCCACAATGGGACAGTACAGCAACAGGACTGTACACCTGACGACGAGCTAAGGA 3041
QY 146 ACTCATTTGCAATGGCAATCATCAGCTCTACGACTTTCATCTTCTCAGTCTGAAGTTAC 205
Db 3042 CTTTCCTTCTCCAGTCTAAATCCCAATGAATCAATGAGTCACTTTTGTCTCAGATTAT 3101
QY 206 GATATATCCC 215
Db 3102 TATATATCCC 3111
RESULT 7
ADK56798/c
ID ADK56798 standard; DNA; 580 BP.
XX
XX AC ADK56798;
XX
XX 06-MAY-2004 (first entry)
XX
XX Plant DNA sequence which confers altered metabolic characteristic #4181.
XX altered metabolic characteristic; plant; acid metabolism;
KW alcohol metabolism; fatty acid metabolism;
KW branched fatty acid metabolism; alkaloid metabolism;
KW amino acid metabolism; ester metabolism; glyceride metabolism;
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW terpene metabolism; isoprenoid metabolism; ketone metabolism;
KW alkyne metabolism; hydrocarbon metabolism; alkene metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
XX Unidentified.
XX
XX WO2003020936-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027884.
XX
XX 31-AUG-2001; 2001US-0316471P.
XX
XX (DOWC) DOW CHEM CO.
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX
XX Novel genes that confer altered metabolic characteristics in Nicotiana
XX benthamiana plants, useful for altering the levels of metabolites e.g.
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
XX Claim 1; SEQ ID NO 4181; 2576pp; English.
XX
XX The invention comprises DNA sequences which confer an altered metabolic
XX characteristic when they are expressed in a plant. The DNA sequences of
XX the invention are useful for producing plants with an altered metabolic
XX characteristic, such as: altered acid metabolism, alcohol metabolism,
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX base metabolism, altered amino acid metabolism, altered ester metabolism,
XX altered glyceride metabolism, altered phenolic metabolism, altered
XX carbohydrate metabolism, altered sterol, oxygenated terpene, or
XX isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX metabolism, ketone or quinone metabolism. The DNA sequences of the
XX invention may be used to provide disease resistance in a plant and gene
XX shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.

XX Sequence 580 BP; 160 A; 102 C; 148 G; 170 T; 0 U; 0 Other;

SQ Query Match 5.7%; Score 35.2; DB 10; Length 580;
Best Local Similarity 53.7%; Pred. No. 1;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 325 TGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTATGAGAGTGGTGGTGGC 384
Db 194 TGGGATGACTAGCTTCCCTTAACACGGCTGAAACCATACTTTGTAGGCCCTTGAATTGC 135

Qy 385 ATATTCCATTGCGAGACTTAAACGGGAACGTTTATCAGCCGGATCTTACTGCTGAGATA 444
Db 134 TTCTTCTCTTTTCCCGAAGTACATAATGACCTGCTCTCTGCAAGCTGCGAGAAGAGAGAA 75

Qy 445 TATGCAATAACAAATT 460
Db 74 TGAAGCAACACAAATT 59

RESULT 8
ID ADS61627 standard; cDNA; 2349 BP.

XX ADS61627;
XX
XX 02-DEC-2004 (first entry)
XX Bacterial polynucleotide #13614.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 37301; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. This sequence represents a bacterial polynucleotide used in
CC production. The sequence improves lignin production or improved galactomannan
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 2349 BP; 799 A; 436 C; 546 G; 568 T; 0 U; 0 Other;

Query Match 5.6%; Score 35; DB 13; Length 2349;
Best Local Similarity 55.3%; Pred. No. 2.3;
Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 292 GACGGATAGGTGAACCCGCAAAATGGTGGTCTTTTGGGTATCAACATCACCATAAGAAAT 351
Db 1330 GACGGACAAGTGGAACACACGGAGTGCCCAATACCGCTCCCATATACAAAAAGGC 1389

Qy 352 GACGGATCCACTCCTATGAGAGTGGTGGTGGTATTCATTTGCAGAACTTAAACGGG 411
Db 1390 AAGGTATCTATGCTAATGGAGGATGAAGTGACATACAGCAAGATGCTCAAACTAAACGCA 1449

Qy 412 AAC 414
Db 1450 AAC 1452

RESULT 9
AAK66772
ID AAK66772 standard; DNA; 42488 BP.

XX AAK66772;
XX
XX 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21584.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.

XX OS
XX WO200157182-A2.
XX
XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.

PR	26-JUL-2000;	2000US-0220363P.	PR	08-NOV-2000;	2000US-0246475P.
PR	26-JUL-2000;	2000US-0220364P.	PR	08-NOV-2000;	2000US-0246476P.
PR	14-AUG-2000;	2000US-0224518P.	PR	08-NOV-2000;	2000US-0246477P.
PR	14-AUG-2000;	2000US-0224519P.	PR	08-NOV-2000;	2000US-0246478P.
PR	14-AUG-2000;	2000US-0225213P.	PR	08-NOV-2000;	2000US-0246523P.
PR	14-AUG-2000;	2000US-0225214P.	PR	08-NOV-2000;	2000US-0246524P.
PR	14-AUG-2000;	2000US-0225266P.	PR	08-NOV-2000;	2000US-0246525P.
PR	14-AUG-2000;	2000US-0225267P.	PR	08-NOV-2000;	2000US-0246526P.
PR	14-AUG-2000;	2000US-0225268P.	PR	08-NOV-2000;	2000US-0246527P.
PR	14-AUG-2000;	2000US-0225270P.	PR	08-NOV-2000;	2000US-0246528P.
PR	14-AUG-2000;	2000US-0225447P.	PR	08-NOV-2000;	2000US-0246532P.
PR	14-AUG-2000;	2000US-0225757P.	PR	08-NOV-2000;	2000US-0246609P.
PR	14-AUG-2000;	2000US-0225758P.	PR	08-NOV-2000;	2000US-0246610P.
PR	14-AUG-2000;	2000US-0225759P.	PR	08-NOV-2000;	2000US-0246611P.
PR	18-AUG-2000;	2000US-0226279P.	PR	08-NOV-2000;	2000US-0246613P.
PR	22-AUG-2000;	2000US-0226681P.	PR	17-NOV-2000;	2000US-0249207P.
PR	22-AUG-2000;	2000US-0226688P.	PR	17-NOV-2000;	2000US-0249208P.
PR	22-AUG-2000;	2000US-0227182P.	PR	17-NOV-2000;	2000US-0249209P.
PR	23-AUG-2000;	2000US-0227009P.	PR	17-NOV-2000;	2000US-0249210P.
PR	30-AUG-2000;	2000US-0228924P.	PR	17-NOV-2000;	2000US-0249211P.
PR	01-SEP-2000;	2000US-0229287P.	PR	17-NOV-2000;	2000US-0249212P.
PR	01-SEP-2000;	2000US-0229343P.	PR	17-NOV-2000;	2000US-0249213P.
PR	01-SEP-2000;	2000US-0229344P.	PR	17-NOV-2000;	2000US-0249214P.
PR	01-SEP-2000;	2000US-0229345P.	PR	17-NOV-2000;	2000US-0249215P.
PR	03-SEP-2000;	2000US-0229509P.	PR	17-NOV-2000;	2000US-0249216P.
PR	05-SEP-2000;	2000US-0229513P.	PR	17-NOV-2000;	2000US-0249217P.
PR	06-SEP-2000;	2000US-0230437P.	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000;	2000US-0230438P.	PR	17-NOV-2000;	2000US-0249244P.
PR	08-SEP-2000;	2000US-0231242P.	PR	17-NOV-2000;	2000US-0249245P.
PR	08-SEP-2000;	2000US-0231243P.	PR	17-NOV-2000;	2000US-0249264P.
PR	08-SEP-2000;	2000US-0231244P.	PR	17-NOV-2000;	2000US-0249265P.
PR	08-SEP-2000;	2000US-0231413P.	PR	17-NOV-2000;	2000US-0249297P.
PR	08-SEP-2000;	2000US-0231414P.	PR	17-NOV-2000;	2000US-0249299P.
PR	08-SEP-2000;	2000US-0232080P.	PR	17-NOV-2000;	2000US-0249300P.
PR	08-SEP-2000;	2000US-0232081P.	PR	01-DEC-2000;	2000US-0250160P.
PR	12-SEP-2000;	2000US-02321968P.	PR	01-DEC-2000;	2000US-0250391P.
PR	14-SEP-2000;	2000US-0232397P.	PR	05-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000;	2000US-0232398P.	PR	05-DEC-2000;	2000US-0251988P.
PR	14-SEP-2000;	2000US-0232399P.	PR	05-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000;	2000US-0232400P.	PR	06-DEC-2000;	2000US-0251479P.
PR	14-SEP-2000;	2000US-0232401P.	PR	08-DEC-2000;	2000US-0251856P.
PR	14-SEP-2000;	2000US-0233063P.	PR	08-DEC-2000;	2000US-0251868P.
PR	14-SEP-2000;	2000US-0233064P.	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000;	2000US-0233065P.	PR	08-DEC-2000;	2000US-0251989P.
PR	21-SEP-2000;	2000US-0234223P.	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000;	2000US-0234274P.	PR	11-DEC-2000;	2000US-0254097P.
PR	25-SEP-2000;	2000US-0234997P.	PR	03-JAN-2001;	2001US-0259678P.
PR	25-SEP-2000;	2000US-0234998P.	XX		
PR	26-SEP-2000;	2000US-0235484P.	XX		
PR	27-SEP-2000;	2000US-0235834P			

PS Claim 1; SEQ ID NO 6745; 15pb; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert

CC polynucleotide that can be used in the recombinant DNA construct of the

CC invention.

XX

SQ Sequence 729 BP; 208 A; 152 C; 171 G; 198 T; 0 U; 0 Other;

Query Match 5.4%; Score 33.8; DB 13; Length 729;

Best Local Similarity 52.5%; Pred. No. 3.4;

Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 461 CAGGACTATTCGACCGACCTCAACCCCTGGTGTCTCATGACGACAAATCTCGTATTG 520

Db 464 CTGGGCATATCTGCACCGGAGTACAAAGCCGAGTGCCTCAACGATGTTAGGAATGGG 523

Qy 521 ATATGCCGGATTTTATGACATATGTCACGTCGGGCGAGCATCTCACTTGTGCTTCCA 580

Db 524 TTTCACGGGATCCCTCTCTGATATTACGTCGTCGAGAGAAATTACGTACGTGCTCCTA 583

Qy 581 TGGGTTTCTTCGGGTCTAGATG 601

Db 584 TGAGTGTAGGCGGACGTACG 604

RESULT 12

ADX12259

ID ADX12259 standard; cDNA; 860 BP.

XX

AC ADX12259;

XX

XX 21-APR-2005 (first entry)

XX

XX Plant full length insert polynucleotide seqid 6834.

XX

XX plant protectant; plant growth regulant; gene therapy; plant;

XX recombinant DNA construct; physical array; plant breeding marker;

XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;

XX growth rate; cell cycle pathway; disease resistance;

XX galactomannan production; lignin production; plant growth regulator;

XX yield; plant growth; plant development; seed oil; protein yield;

XX protein content; gene; ss.

XX

XX Unidentified.

XX

XX US2004034888-A1.

XX

XX 19-FEB-2004.

XX

XX 28-APR-2003; 2003US-00425114.

XX

XX 06-MAY-1999; 99US-00304517.

XX

XX 05-NOV-2001; 2001US-00985678.

XX

XX (LIUJ/) LIU J.

XX

XX (ZHOU/) ZHOU Y.

XX

XX (KOVA/) KOVALIC D K.

XX

PA (SCRE/) SCREEN S E.

PA (TAB/) TABASKA J E.

XX (CAOY/) CAO Y.

XX

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX

XX Claim 1; SEQ ID NO 6834; 15pb; English.

XX

XX The invention describes a recombinant DNA construct comprising a

XX polynucleotide consisting of a sequence encoding an amino acid sequence

XX available in electronic form from the US patent office at

XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

XX of the invention are also useful in physical arrays of molecules and as

XX plant breeding markers. The recombinant DNA construct is useful for

XX improving plant tolerance to cold, heat, drought, herbicides, extreme

XX osmotic conditions, pathogens or pests, for manipulating growth rate in

XX plant cells by modification of the cell cycle pathway, for conferring

XX increased resistance to plant disease, for producing galactomannan,

XX lignin or plant growth regulators, for increasing the rate of homologous

XX recombination in plants, for improving yield by modification of

XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

XX or by providing improved plant growth and development under at least one

XX stress condition or for modifying seed oil or protein yield and/or

XX content. This sequence represents a plant full length insert

XX polynucleotide that can be used in the recombinant DNA construct of the

XX invention.

XX

SQ Sequence 860 BP; 220 A; 204 C; 245 G; 191 T; 0 U; 0 Other;

Query Match 5.4%; Score 33.8; DB 13; Length 860;

Best Local Similarity 52.5%; Pred. No. 3.6;

Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 461 CAGGACTATTCGACCGACCTCAACCCCTGGTGTCTCATGACGACAAATCTCGTATTG 520

Db 600 CTGGGCATATCTGCACCGGAGTACAAAGCCGAGTGCCTCAACGATGTTAGGAATGGG 659

Qy 521 ATATGCCGGATTTTATGACATATGTCACGTCGGGCGAGCATCTCACTTGTGCTTCCA 580

Db 660 TTTCACGGGATCCCTCTCTGATATTACGTCGTCGAGAGAAATTACGTACGTGCTCCTA 719

Qy 581 TGGGTTTCTTCGGGTCTAGATG 601

Db 720 TGAGTGTAGGCGGACGTACG 740

RESULT 13

ADK56319/c

ID ADK56319 standard; DNA; 706 BP.

XX

XX ADK56319;

XX

XX 06-MAY-2004 (first entry)

XX

XX Plant DNA sequence which confers altered metabolic characteristic #3702.

XX

XX altered metabolic characteristic; plant; acid metabolism;

XX alcohol metabolism; fatty acid metabolism;

XX branched fatty acid metabolism; alkaloid metabolism;

XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;

XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX

XX Unidentified.

OS

WO2003020936-A1.
13-MAR-2003.
30-AUG-2002; 2002WO-US027884.
31-AUG-2001; 2001US-0316471P.
(DOWC) DOW CHEM CO.
(DOWC) DOW AGROSCIENCES LLC.
Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
Orliedo JVB, Croasley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
WPI; 2003-313091/30.
Novel genes that confer altered metabolic characteristics in Nicotiana
benthiana plants, useful for altering the levels of metabolites e.g.
acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
Claim 1; SEQ ID NO 3702; 2576pp; English.
The invention comprises DNA sequences which confer an altered metabolic
characteristic when they are expressed in a plant. The DNA sequences of
the invention are useful for producing plants with an altered metabolic
characteristic, such as: altered acid metabolism, alcohol metabolism,
fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
base metabolism, altered amino acid metabolism, altered ester metabolism,
altered glyceride metabolism, altered phenolic metabolism, altered
carbohydrate metabolism, altered sterol, oxygenated terpene, or
isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
metabolism, ketone or quinone metabolism. The DNA sequences of the
invention may be used to provide disease resistance in a plant and gene
shuffling or sexual PCR procedures. The present nucleic acid represents a
DNA sequence of the invention.
Sequence 706 BP; 180 A; 163 C; 143 G; 220 T; 0 U; 0 Other;

Query Match	5.4%;	Score 33.4;	DB 10;	Length 706;
Best Local Similarity	47.4%;	Pred. No. 4.5;		
Matches 100;	Conservative 0;	Mismatches 111;	Indels 0;	Gaps 0;
Qy	233	AGGTAGGAGACTTCGAAATTAGAGTTAACTCCCTCGACGAGTTAAAGAGTGTGGGGTACG	292	
Db	578	ATGCAGGACGCTTCAGTATTTTGTGCATCCCACTCTTCATTGTAAGTGTATGATCCCA	519	
Qy	293	ACGGGATAGGTGAAACCGCAAAATGGTGGTTTTGGGTTATCAACATCACCAATAGAAATG	352	
Db	518	GGTGGAGTAAATCCAGGCAACTCTTGTGAGTGGGAAATCAAAAATCACCGAAAGCTGGG	459	
Qy	353	ACGGATCCACTCCTATGGAGTGCCTGATGGCATATTCCAATTCGACGAACCTTAAACGGGA	412	
Db	458	CACAGTGTCTCTTTACATAGGTCCATGGCCCTGTGGTGGACATGGAAAGAACAAATAGTTA	399	
Qy	413	ACGTTTATCAGCCGGATTCTACTGCTGAGAT	443	
Db	398	ACATCAATCACAGCTTTCTTCGGGTGAGAT	368	

RESULT 14
ADA71938
ID ADA71938 standard; DNA; 2000 BP.

20-NOV-2003 (first entry)

Rice gene, SEO ID 5263.

Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene: ds.

OS	Oryza sativa.
XX	
FN	WO2003000898-A1.
XX	
PD	03-JAN-2003.
XX	
PP	22-JUN-2001; 2001WO-IB001105.
XX	
PR	22-JUN-2001; 2001WO-IB001105.
XX	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.
XX	
PI	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI	Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX	
DR	WPI; 2003-175290/17.
XX	
PT	Identifying at least one gene involved in plant resistance or response to
PT	pathogenic infection for conferring resistance or tolerance to a plant to
PT	bacterial, fungal or viral infection by determining or detecting plant
PT	gene expression.
XX	
PS	Claim 27; SEQ ID NO 5263; 899pp; English.
XX	
CC	The present invention relates to a method (M1) for identifying genes
CC	involved in plant resistance or response to pathogenic infection. M1
CC	comprises identifying a gene whose expression is significantly altered in
CC	the incompatible interaction of plant gene expression relative to
CC	expression of the gene in an uninfected plant, in a mutant plant that
CC	does not express a gene associated with response to pathogenic infection,
CC	or in a corresponding incompatible or compatible interaction. (M1) is
CC	useful for conferring resistance to resistance or tolerance to a plant to
CC	bacterial, fungal or viral infection. The present sequence was used to
CC	illustrate the invention.
XX	
SQ	Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

[illegible]

QY 478 GACCTCAACCCCT 489
: : : : :
Db 576 SKCSWYCKMSYY 587

RESULT 15
ID ADP25286/c
ADP25286 standard; cDNA; 7480 BP.
XX AC ADP25286;
XX XX
DT 18-NOV-2004 (first entry)
XX XX
XX PRO polypeptide encoding cDNA SEQ ID NO:2464.
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antiporiatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX XX
OS Unidentified.
XX XX
PN WO2004041170-A2.
XX XX
PD 21-MAY-2004.
XX XX
PP 30-OCT-2003; 2003WO-US034312.
XX XX
PR 01-NOV-2002; 2002US-0423394P.
XX XX
PA (GETH) GENENTECH INC.
XX XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX XX
DR WPI; 2004-419628/39.
XX XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX XX
XX Claim 1; SEQ ID NO 2464; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy. Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polynuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX disease, asthma, allergic rhinitis, atopic dermatitis, food
XX hypersensitivity, urticaria, an immunologic disease of the lung,
XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX pneumonitis, a transplantation associated disease, graft rejection or
XX graft-versus-host disease. The present sequence encodes a PRO protein of
XX the invention.

XX Sequence 7480 BP; 2277 A; 1271 C; 1472 G; 2460 T; 0 U; 0 Other;

Query Match 5.3%; Score 33.2; DB 13; Length 7480;
Best Local Similarity 44.8%; Pred. No. 15;
Matches 128; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 18 TCAGAGAAACACACCGCGGAACGCATCAACGGTAAGCGCTACAACTTCTTTGGTTAATTC 77
Db 2442 TAGATGGAAGAAACTGCCAAAAGCACCATTCTTACTCCAAATCCATATCTTAAGTAATTC 2383
QY 78 GACGAATAGTTTCACAGGTAGCAAGCAAGCAAACTCGAGTACGTCTCCCGTCATAA 137
Db 2382 TTTAGAAAATTAAGAAATAAAAAAAGTAAATACACACAAAAGATCTTATCCAAATGCTT 2323
QY 138 GTCTACGAACCTCATTTGCAACATCGCAACATCAAGCTGTCTACGACTTTCATCTTCTCAGTC 197
Db 2322 GCTTCTATACAACTTAATGTATGTATTAATCTTATTAATTTACGGCTTATGATGCAGATTT 2263
QY 198 GAAAGTTACGATATATCCCGTTTTCACACATACGGGAAGGTAGGAGACTTGGAAATTAAGAT 257
Db 2262 GAATATCCTAAATAACATTTTCCCAACAAATCAGGTATGGAGCATAAAAGTATCATAAAGGT 2203
QY 258 TAACTCCCTCGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGT 303
Db 2202 ATAACCTCTCGACGAGGTGCCAGTCTCTGTGTGTCCTCAACACAGCAGCAGT 2157

Search completed: April 12, 2006, 08:35:25

Job time : 494 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	39.8	6.4	444	1	AU269824	AU269824
C 2	39.6	6.4	714	6	CA968800	CA968800
C 3	39.2	6.3	729	5	AU445212	AU445212
C 4	39.2	6.3	729	5	BJ364247	BJ364247
C 5	39.2	6.3	782	3	CA968800	CA968800
C 6	39	6.3	393	3	CA968800	CA968800
C 7	39	6.3	742	8	CA968800	CA968800
8	39	6.3	782	7	CA968800	CA968800
C 9	38.6	6.2	371	3	CA968800	CA968800
C 10	38.6	6.2	374	3	CA968800	CA968800
C 11	38.6	6.2	393	3	CA968800	CA968800
C 12	38.6	6.2	393	3	CA968800	CA968800
C 13	38.6	6.2	394	3	CA968800	CA968800
C 14	38.6	6.2	422	3	CA968800	CA968800
C 15	38.6	6.2	458	3	CA968800	CA968800
C 16	38.6	6.2	463	3	CA968800	CA968800
C 17	38.6	6.2	463	3	CA968800	CA968800
C 18	38.6	6.2	470	3	CA968800	CA968800
C 19	38.6	6.2	472	3	CA968800	CA968800
C 20	38.6	6.2	503	3	CA968800	CA968800
C 21	38.6	6.2	506	3	CA968800	CA968800
C 22	38.6	6.2	522	3	CA968800	CA968800

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QY 359 CCACTCCTAGGAGTGGTGGATATTCATTTGCAGAACTTAAACGGGAACGTTT 418
Db 130 CTTTGTGTAATGATCNCAGGTTGGTTAGCTTACATTAATAAGGGTATGTTAAAGATG 189
QY 419 ATCAGCGGAGTTCTACTGCTGAGATATATGCAATACAAATTCAGGAGCTATT 471
Db 190 CAACCTTCAATGTTTACTGCTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 242

RESULT 2
CA996800/c
LOCUS
DEFINITION
  iq03d03.y1 Meloidogyne hapla J2 pamp1 v1 Meloidogyne hapla cDNA 5'
  similar to TR:001685 001685 SIMILAR TO ALANINE AMINOTRANSFERASE.
  [] ; mRNA sequence.
ACCESSION
  CA996800
VERSION
  CA996800.1 GI:27541671
KEYWORDS
  EST.
SOURCE
  Meloidogyne hapla
  Meloidogyne hapla
  Meloidogyne hapla
  Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
  Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
REFERENCE
  1 (bases 1 to 714)
  McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
  Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
  Bowers,Y., Gibbons,M., Ritter,B., Bennett,J., Franklin,C., Beck,C.,
  Teagareishvili,R., Konko,I., Kennedy,S., Maguire,L., Beck,C.,
  Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
  Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
  McCann,R., Waterston,R. and Wilson,R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  The library was constructed by Claire Murphy and Dr. James McCarter
  at Washington University, St. Louis. J2 were provided by Dr.
  Valerie Williamson of the University of California at Davis
  (vmwilliamson@ucdavis.edu).
  Seq primer: -40RP from Gibco
  High quality sequence stop: 414.
FEATURES
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  /note="Vector: pamp1 (Gibco); Site 1: NotI; Site 2: SalI;
  The library was constructed by Claire Murphy and Dr. James
  McCarter at Washington University, St. Louis. The cDNA was
  made by using Dynabead oligo-dr priming (Dynal). PCR based
  library using a modified protocol from the SMART PCR cDNA
  Synthesis Kit from Clontech. Directionally cloned into the
  UDG sites of pamp1. J2 were provided by Dr. Valerie
  Williamson of the University of California at Davis
  (vmwilliamson@ucdavis.edu)."

QY 320 CGTTTGGTGTATCAACATCAACATAAGAAATGACGATCCACTCTATGAGGTGCTTG 379
Db 268 CATTGGATTAACTGCTCTCAACAGTAAGCACACGCTTTTCCTGCCAAATTTGAACCTGGTTG 209
QY 380 ATGGCATATTCATTTGTCAGAACTTAAACGGGAACGTTTATCAGCCGGAATTCCTACTGCTG 439

Query Match 6.4%; Score 39.6; DB 6; Length 714;
Best Local Similarity 50.5%; Pred. No. 0.46;
Matches 96; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 320 CGTTTGGTGTATCAACATCAACATAAGAAATGACGATCCACTCTATGAGGTGCTTG 379
Db 268 CATTGGATTAACTGCTCTCAACAGTAAGCACACGCTTTTCCTGCCAAATTTGAACCTGGTTG 209
QY 380 ATGGCATATTCATTTGTCAGAACTTAAACGGGAACGTTTATCAGCCGGAATTCCTACTGCTG 439

Query Match 6.4%; Score 39.2; DB 3; Length 475;
Best Local Similarity 51.4%; Pred. No. 0.55;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 299 TAGTGAAACGGCAAAATGGTGGCTTTGGGTTATCAACATCACCATAAGAAATGACGGAT 358
Db 269 TGGTTGAAAAGAAAATAAAAGTTAATGATATCAACAAACCGTATTATATGTCGAAT 210
QY 359 CCAGTCTCTATGAGGAGTGGTTGATGGCATATTTCCATTTTCAGAACTTAAACCGGAACGTTT 418
Db 209 CTTTGTGTAATGATCACCAGGTTGGTTAGCTTACATTAATAAGGGTATTTGGTAAAGATG 150
QY 419 ATCAGCCGGAATTCCTACTGCTGAGATATATGCAATACAAATTCAGGAGCTATT 471
Db 149 CAACCTTCAATGTTTACTGCTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 97

RESULT 4
BU364247/c
LOCUS
DEFINITION
  BU364247 CSEQHN72 Gallus gallus cDNA clone CHEST740x15 5', mRNA
  sequence.
ACCESSION
  BU364247
VERSION
  BU364247.1 GI:25872248
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)

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Db 208 TTGCATATTTCTGTTTATTTCACAATTTAAATTTGGTAAAGTCTTGTGTTGGCTG 149
QY 440 AGATATATGAATAATCAAAATTCAGGAGCTATTTCGACCGACCTCAACCCCTGGTGTGCCA 499
Db 148 GAATATAAGTAAACACAGACAGTCGATATAATGCTGCTCAATCTCAAAGCTGTTGAATGCA 89
QY 500 TGACGACAAA 509
Db 88 TTCAAAAAAA 79

RESULT 3
BJ445212/c
LOCUS
DEFINITION
  BJ445212 Dictyostelium discoideum cDNA library, VF Dictyostelium
  discoideum cDNA clone ddv58e21 3', mRNA sequence.
ACCESSION
  BJ445212
VERSION
  BJ445212.1 GI:19419933
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum
  Dictyostelium discoideum
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 475)
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
  Full length cDNA of Dictyostelium discoideum at the vegetative
  stage
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
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ORIGIN
  Query Match 6.3%; Score 39.2; DB 3; Length 475;
  Best Local Similarity 51.4%; Pred. No. 0.55;
  Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 299 TAGTGAAACGGCAAAATGGTGGCTTTGGGTTATCAACATCACCATAAGAAATGACGGAT 358
Db 269 TGGTTGAAAAGAAAATAAAAGTTAATGATATCAACAAACCGTATTATATGTCGAAT 210
QY 359 CCAGTCTCTATGAGGAGTGGTTGATGGCATATTTCCATTTTCAGAACTTAAACCGGAACGTTT 418
Db 209 CTTTGTGTAATGATCACCAGGTTGGTTAGCTTACATTAATAAGGGTATTTGGTAAAGATG 150
QY 419 ATCAGCCGGAATTCCTACTGCTGAGATATATGCAATACAAATTCAGGAGCTATT 471
Db 149 CAACCTTCAATGTTTACTGCTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 97

RESULT 4
BU364247/c
LOCUS
DEFINITION
  BU364247 CSEQHN72 Gallus gallus cDNA clone CHEST740x15 5', mRNA
  sequence.
ACCESSION
  BU364247
VERSION
  BU364247.1 GI:25872248
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)

```

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ORGANISM      Gallus gallus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
TITLE          Phasianidae; Gallus.
JOURNAL        1 (bases 1 to 729)
PUBMED         Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
COMMENT        Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
                A Comprehensive Collection of Chicken cDNAs
                Curr. Biol. 12 (22), 1965-1969 (2002)
                12445392
                Contact: Simon Hubbard
                Department of Biomolecular Sciences
                University of Manchester Institute of Science and Technology
                (UMIST)
                PO Box 88, Manchester, M60 1QD, UK
                Tel: 0161208930
                Fax: 01612360409
                Email: Simon.Hubbard@umist.ac.uk.

FEATURES      source
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               /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
               EcoRI; Site_2: NotI; This normalized library was
               constructed from 1 million independent clones. cDNA
               synthesis was initiated using an oligo(dT) primer, using
               methylated C in the first strand synthesis reaction.
               Following this first strand reaction, double-stranded cDNA
               was blunted, ligated to NotI adapters, digested with
               EcoRI, size-selected, and cloned into the NotI and EcoRI
               compatible sites of a custom modified MCS of the
               pBluescript (KS+) vector. The library was normalized in 2
               rounds using conditions adapted from Soares et al., PNAS
               (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
               (1996): 791, except that a significantly longer
               reannealing hybridization was used."

ORIGIN
Query Match      6.3%; Score 39.2; DB 5; Length 729;
Best Local Similarity 52.4%; Pred. No. 0.63;
Matches 86; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 62 CTTCTTTGGTTAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTA 121
Db 387 CTTATTAGTGACTGTGTGCAATAGTTCACAAGATGTAGATGACAGCATAGTAAGGA 328
Qy 122 CGTCTCCGCTCATAGTCTCAGAACTCATTTGCAACATGCGCAACATCAAGTGTCTAGA 181
Db 327 AGACACCCGACCCCTCCAGAAAAGTGCCCTGCAACTCGTGAAGCCTTCAGCAGCGGGA 268
Qy 182 CTTGATCTTCTCAGTCGAGGTACGATATATCCCGTTTCACACA 225
Db 267 AGTCAACCTGTGATAGTAACATTTTGTTCGCCCACTTCATTCA 224

RESULT 5
BJ436673/c
LOCUS          BJ436673 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION    BJ436673 Dictyostelium discoideum cDNA clone ddd31120 3', mRNA sequence.
ACCESSION     BJ436673
VERSION       BJ436673.1 GI:19411395
KEYWORDS      EST.
SOURCE        Dictyostelium discoideum
ORGANISM      Dictyostelium discoideum

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 729)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 0161208930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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               /lab_host="DH10B"
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               /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
               EcoRI; Site_2: NotI; This normalized library was
               constructed from 1 million independent clones. cDNA
               synthesis was initiated using an oligo(dT) primer, using
               methylated C in the first strand synthesis reaction.
               Following this first strand reaction, double-stranded cDNA
               was blunted, ligated to NotI adapters, digested with
               EcoRI, size-selected, and cloned into the NotI and EcoRI
               compatible sites of a custom modified MCS of the
               pBluescript (KS+) vector. The library was normalized in 2
               rounds using conditions adapted from Soares et al., PNAS
               (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
               (1996): 791, except that a significantly longer
               reannealing hybridization was used."

ORIGIN
Query Match      6.3%; Score 39.2; DB 5; Length 729;
Best Local Similarity 52.4%; Pred. No. 0.63;
Matches 86; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 62 CTTCTTTGGTTAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTA 121
Db 387 CTTATTAGTGACTGTGTGCAATAGTTCACAAGATGTAGATGACAGCATAGTAAGGA 328
Qy 122 CGTCTCCGCTCATAGTCTCAGAACTCATTTGCAACATGCGCAACATCAAGTGTCTAGA 181
Db 327 AGACACCCGACCCCTCCAGAAAAGTGCCCTGCAACTCGTGAAGCCTTCAGCAGCGGGA 268
Qy 182 CTTGATCTTCTCAGTCGAGGTACGATATATCCCGTTTCACACA 225
Db 267 AGTCAACCTGTGATAGTAACATTTTGTTCGCCCACTTCATTCA 224

RESULT 5
BJ436673/c
LOCUS          BJ436673 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION    BJ436673 Dictyostelium discoideum cDNA clone ddd31120 3', mRNA sequence.
ACCESSION     BJ436673
VERSION       BJ436673.1 GI:19411395
KEYWORDS      EST.
SOURCE        Dictyostelium discoideum
ORGANISM      Dictyostelium discoideum
```

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ORGANISM      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE      1 (bases 1 to 782)
AUTHORS        Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE          Full length cDNA of Dictyostelium discoideum at the vegetative
                stage
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.

FEATURES      source
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ORIGIN
Query Match      6.3%; Score 39.2; DB 3; Length 782;
Best Local Similarity 51.4%; Pred. No. 0.65;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTGCCTTTGGGTTATCAACATCACCATAGRAATGACCGAT 358
Db 425 TGGTTGAAAAGAATAAATAAAGTTAATGATATCAACAAACCGTATTAGATGCGAAT 366
Qy 359 CCACCTCTATGGAGGTGCTTGATCGCATATTCCTATTTGCAGAACTTAAACCGGAACGTTT 418
Db 365 CTTTGTGTTATGATCACCAGGTGGTTAGCTTACATTAAATGGGTATNGTTAAGATG 306
Qy 419 ATCAGCCGGATTCCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
Db 305 CAACCTCAATGTTTACTTACTGCTGAGATTTATGCTCATTCAATGCTGCTAAAAAT 253

RESULT 6
BJ439058/c
LOCUS          BJ439058 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION    BJ439058 Dictyostelium discoideum cDNA clone ddd39f08 3', mRNA sequence.
ACCESSION     BJ439058
VERSION       BJ439058.1 GI:19413780
KEYWORDS      EST.
SOURCE        Dictyostelium discoideum
ORGANISM      Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 393)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES      source
               1..393
               /organism="Dictyostelium discoideum"
               /mol_type="mRNA"
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/dev stage="Growth phase"
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Query Match      6.3%; Score 39; DB 3; Length 393;
Best Local Similarity 50.0%; Pred. No. 0.6;
Matches 84; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAATGGTGGCTTTGGGTATCAATCACCATAAGAAATGACGGAT 358
Db 255 TGGTTGAAAAGNAATAAAAGAAATTAATGATNATCAACAAACCGTATTAGATGNGAAT 196
Qy 359 CCACTCTATGGAGTGGTGGTATGCGCATATTCCTATTTGCAGAACTTAAACCGGGAACGTTT 418
Db 195 CTTTGTATGATCNCACCGAGTGGTTAGCTTACNNTAATGATGGTATTTGGTAAAGATG 136
Qy 419 ATCAGCGGATTCCTACTGCTGAGATATATGCAAAATACAAATTCAGGGA 466
Db 135 CAATTCNATGTTACTTGGTGAAGTTTATGCTCATTCAAANGCTGNTA 88

RESULT 7
DR070622
LOCUS      RTDK1_14_C03_g1_A029 Roots, dark Pinus taeda cDNA clone
DEFINITION RTDK1_14_C03_g1_A029 5', mRNA sequence.
ACCESSION  DR070622.1 GI:67048356
VERSION     EST.
KEYWORDS    Pinus taeda (loblolly pine)
SOURCE      Pinus taeda
ORGANISM    Pinus taeda
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Pratt, L., Cordonnier-Pratt, M.M., Lorenz, W.W., Zimmermann, C. and
Dean, J.F.D.
An EST database from dark-treated loblolly pine (Pinus taeda) roots
Unpublished (2005)
Other ESTs: RTDK1_14_C03_b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of
Forest Resources, University of Georgia); plant material prepared
by Craig Zimmermann (School of Forest Resources, University of
Georgia) using rooted cuttings provided by the Forest Biology
Research Cooperative (FBRC) and the CCLONES project at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGAAACAGCTATGACC).
FEATURES             source
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        /strain="3 CCLONES"
        /db_xref="taxon:3352"
        /clone="RTDK1_14_C03_A029"
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        /clone_lib="Roots, dark"
        /note="Organ: Root; Vector: pSL1180; Site 1: ECORI;
Site 2: XhoI; The library was prepared from polyA+ RNA
from the roots of 1-year-old loblolly pine (Pinus taeda)
cuttings that were rooted and then planted in washed sand.
The rooted cuttings were maintained for 50 days (May 1
2003 harvest) under ambient conditions in a local
greenhouse. They were kept on a weekly regimen of 0.5x

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ORIGIN
Query Match      6.3%; Score 39; DB 8; Length 742;
Best Local Similarity 58.0%; Pred. No. 0.74;
Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 275 TTAAGAGTGGGTACGACGGATAGTGTAACCGCAAAATGGTGGCTTTGGGTATCA 334
Db 138 TTAAGAGTGGGTACGTCGGGAAGGAGTCTTTTTTTGGCTTTTCAAGATGCA 197
Qy 335 ACATCACCATAAGAAATGACGGATCCACTCTCTATGGAGGTGTTTGATGGCATATTTCCAT 393
Db 198 AACAGGGAAGTGACATGTCGTCCCAACAATTAAGGAGCGCTTAAGGCAGTCTCCAT 256

RESULT 8
COI67205
LOCUS      FLD1_67_C04_g1_A029 Root flooded Pinus taeda cDNA clone
DEFINITION FLD1_67_C04_g1_A029 5', mRNA sequence.
ACCESSION  COI67205
VERSION     GI:48937746
KEYWORDS    Pinus taeda (loblolly pine)
SOURCE      Pinus taeda
ORGANISM    Pinus taeda
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C.,
Johnson, H., Anfuso, C., Kamran, D., Chhabra, D. and Dean, J.F.D.
A loblolly pine (Pinus taeda) EST database from flooded roots
Unpublished (2004)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of
Forest Resources, University of Georgia); plant material prepared
by Craig Zimmermann (School of Forest Resources, University of
Georgia) using rooted cuttings provided by the Forest Biology
Research Cooperative (FBRC) and the CCLONES project at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGAAACAGCTATGACC).
FEATURES             source
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        /clone_lib="Root flooded"
        /note="Organ: root; Vector: pSL1180; Site 1: ECORI;
Site 2: XhoI; The library was prepared from polyA+ RNA
from the roots of 1-year-old loblolly pine (Pinus taeda)
cuttings that were rooted and then planted in washed sand.
Prior to harvesting tissues for RNA isolation, the rooted
cuttings were maintained for 27 days (April 2003) under

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nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Twenty-four hours (24h) prior to harvesting roots for mRNA preparation, the potted trees were placed in a dark growth chamber at 25 C. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain 5% soil moisture content. Pots holding the rooted cuttings were fully submerged in water for 24 hours prior to harvest of the roots for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

	Query Match	6.3%	Score 39	DB 7	Length 782	
	Best Local Similarity	58.0%	Pred. No. 0.75			
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Qy	275	TTAAGACTGTGGGGTACGACGGGATAGGTGAACCGCAATGGTGCCTTTTGGGGTTATCA	334			
Db	284	TTAAAAGTGGGGATACGTCGGGAAGGGAAGTCTCTTTTCTGCTCTTCAAGGATGCA	343			
Qy	335	ACATCACCATAAGAAATGACGGATCCACTCCTATGGAGGTCGTTGATGGCATATTCGAT	393			
Db	344	AACAGGGAAGGTGACATGTCGTCCCAACAANTTAAGGAGGCGGTTAAGGGCAGTCTCCAT	402			

RESULT	9
LOCUS	BJ440426/c
LENGTH	371 bp
DEFINITION	Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv43116 3', mRNA sequence.
ACCESSION	BJ440426
VERSION	BJ440426.1 GI:19415148
KEYWORDS	EST.
SOURCE	Dictyostelium discoideum
ORGANISM	Dictyostelium discoideum
REFERENCE	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. 1 (bases 1 to 371)
AUTHORS	Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE	Full length cDNA of Dictyostelium discoideum at the vegetative

Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .371

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FEATURES
source
1. .371
Location/Qualifiers
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/mol_type="mRNA"
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Qy	299 TAGGTGAACCGCAAAATGGTTCGTTTTGGGTTATCAACATCACCATAGAAGAAATGACGGAT	358	
Dd	252 TGGTTGAARAAGAAATAAAAANGTTAATGATATCAACAACCGTATTAGATGTGCAT	193	
Qy	359 CCACCTCCTATGGAGTGCTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTT	418	
Dd	192 CTTTGTGTAATGATCACCCAGGTGGTTTACTTTACATTAAAAITGGGTATTGGTAAAGATG	133	
Qy	419 ATCAGCGGATTTCTACTGCTGAGATATATGCAAAATCAAATTCAGGACCTATT	471	

Db	132	CAACTTCATGTTTACTGGTGAAGTTATGCTCATTCAAATGCTGCTAAAAAT	80
RESULT 10			
BJ440571/c			
LOCUS			
DEFINITION	BJ440571 Dictyostelium discoideum cDNA library, VF	374 bp	EST 13-MAR-2002
	discoideum cDNA clone ddv44:05 3', mRNA sequence.		

ACCESSION	BJ440571
VERSION	BJ440571.1
KEYWORDS	GI:19415293
SOURCE	EST.
ORGANISM	Dictyostelium discoideum
REFERENCE	Dictyostelium discoideum
AUTHORS	Dictyostelium discoideum
TITLE	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. (bases 1 to 374)
JOURNAL	Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
COMMENT	Full length cDNA of Dictyostelium discoideum at the vegetative stage Unpublished (2002) Contact: Tadasu Shin-i

Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhin@genes.nig.ac.jp
Location/Qualifiers
1. .374

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/organism="Dictyostelium discoideum"
/mol_type="mRNA"
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	Best Local Similarity	51.4%;	Pred. No. 0.8;		
	Matches	89;	Conservative	0;	Mismatches 84; Indels 0; Gaps 0;
Qy	299	TAGGTGAAACCGCAAAATGGTCGTTTTGGGTTATCAACATCACCATAAGAAATGACGGAT	358		
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Qy	359	CCACTCCTATGGAGGTCGTTTGATGGCATATTCATTTCGAGAACTTTAAACGGGAACGTTT	418		
Db	196	CTTTTGTTAATGATCAACCCAGTGGTTAGCTTACATTAAATGGGTATTGGTAAAGATG	137		
Qy	419	ATCAGCGGGATTCCTACTGCTGAGATATATGCAAAATACAAATTCAGGACTATT	471		
Db	136	CAACTTCAATGTTTATCTGGTGAAGTTTATGCTCATTCAAATGCTGCTAAAAT	84		

RESULT 11	
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LOCUS	391 bp mRNA linear EST J3-MAR-2002
DEFINITION	Dictyostelium discoidaeum cDNA library, VF Dictyostelium discoidaeum cDNA clone dcdv44m07 3', mRNA sequence.
ACCESSION	Bj440677
VERSION	Bj440677
KEYWORDS	GI:19415399
SOURCE	EST.
ORGANISM	Dictyostelium discoideum Dictyostelium discoideum Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. 1 (bases 1 to 391)
REFERENCE	Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
AUTHORS	Full length cDNA of Dictyostelium discoideum at the vegetative stage
TITLE	Unpublished (2002)
JOURNAL	Contact: Tadasu Shin-i
COMMENT	Center For Genetic Resource Information


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SOURCE      Dictyostelium discoideum
ORGANISM     Dictyostelium discoideum
REFERENCE    Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
AUTHORS      1 (bases 1 to 422)
TITLE        Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
              Full length cDNA of Dictyostelium discoideum at the vegetative
              stage
JOURNAL      Unpublished (2002)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshini@genes.nig.ac.jp.
FEATURES     source
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Best Local Similarity 51.4%; Pred. No. 0.83;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 299 TAGGTGAACCGCAAAATGGTCGGTTTGGGTTATCAACATCACCATAAGAATGACGGAT 358
Db 247 TGGTTGAAAAAGAAAAAAGTTAATGATAATCAACAAAACCGTATTAGATGTCGAAT 188
Qy 359 CCACCTCCCTATGGAGTGGTTGATGGCATATTCATTTCAGAACTTAAACGGGAACGTTT 418
Db 187 CTTTGTGTTAATGATCACCAGGTGGTTTAGCTTACATTAAATGGGTATTGGTAAAGATG 128
Qy 419 ATCAGCGCGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
Db 127 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCAATGCTCTAAAAAT 75

RESULT 15
BJ444052/c
LOCUS        BJ444052      458 bp      mRNA      linear      EST 13-MAR-2002
DEFINITION   BJ444052 Dictyostelium discoideum cDNA library, VF Dictyostelium
              discoideum cDNA clone ddv55f06 3', mRNA sequence.
ACCESSION    BJ444052.1 GI:19418773
VERSION      BJ444052
KEYWORDS     EST.
SOURCE       Dictyostelium discoideum
ORGANISM     Dictyostelium discoideum
              Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE    1 (bases 1 to 458)
AUTHORS      Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE        Full length cDNA of Dictyostelium discoideum at the vegetative
              stage
JOURNAL      Unpublished (2002)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshini@genes.nig.ac.jp.
FEATURES     source
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                location/Qualifiers
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                /mol_type="mRNA"
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Best Local Similarity 51.4%; Pred. No. 0.85;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 299 TAGGTGAACCGCAAAATGGTCGGTTTGGGTTATCAACATCACCATAAGAATGACGGAT 358
Db 254 TGGTTGAAAAAGAAAAAAGTTAATGATAATCAACAAAACCGTATTAGATGTCGAAT 195
Qy 359 CCACCTCCCTATGGAGTGGTTGATGGCATATTCATTTCAGAACTTAAACGGGAACGTTT 418
Db 194 CTTTGTGTTAATGATCACCAGGTGGTTTAGCTTACATTAAATGGGTATTGGTAAAGATG 135
Qy 419 ATCAGCGCGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
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Job time : 3497 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 07:23:05 ; Search time 174 Seconds
(without alignments)
6344.056 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.8	5.4	601	3	US-09-949-016-150404
2	33.8	5.4	181251	3	US-09-949-016-15970
C 3	33.4	5.4	421118	3	US-09-949-016-16297
4	32.4	5.2	285478	3	US-09-949-016-13362
C 5	32.2	5.2	1141	3	US-09-806-708B-22
6	32	5.2	832	3	US-09-621-976-2813
C 7	32	5.2	99304	3	US-09-949-016-15440
C 8	31.4	5.1	17000	3	US-09-679-299A-18
C 9	31.4	5.1	236964	3	US-09-949-016-15753
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C 11	30.8	5.0	1995	3	US-09-710-279-1257
C 12	30.8	5.0	2169	3	US-09-134-001C-2645
C 13	30.8	5.0	3356	3	US-09-710-279-3920
14	30.6	4.9	3001	3	US-09-539-333D-185
C 15	30.4	4.9	601	3	US-09-949-016-151347
C 16	30.4	4.9	601	3	US-09-949-016-151410
17	30.4	4.9	3509	3	US-09-949-016-4254
18	30.4	4.9	3509	3	US-09-949-016-4255
19	30.4	4.9	118382	3	US-09-949-016-15996
20	30.4	4.9	118382	3	US-09-949-016-15997
21	30.2	4.9	1194	3	US-09-270-767-5598
22	30.2	4.9	1194	3	US-09-270-767-20880
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C 24	30	4.8	601	3	US-09-949-016-128578

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C 27	30	4.8	1270	3	US-09-415-277C-16	Sequence 16, Appli
C 28	30	4.8	1271	3	US-09-415-277C-3	Sequence 3, Appli
29	30	4.8	24205	3	US-09-949-016-15385	Sequence 15385, A
30	29.8	4.8	351	3	US-09-248-796A-2992	Sequence 2992, Ap
31	29.8	4.8	947	3	US-09-640-211A-138	Sequence 138, App
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34	29.8	4.8	2090	3	US-09-270-767-4280	Sequence 4280, Ap
35	29.8	4.8	2090	3	US-09-270-767-19562	Sequence 19562, A
36	29.8	4.8	5619	3	US-09-799-451-241	Sequence 241, App
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C 41	29.6	4.8	7917	2	US-08-167-854-1	Sequence 1, Appli
42	29.6	4.8	678533	3	US-09-949-016-14577	Sequence 14577, A
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45	29.4	4.7	1211	3	US-08-858-207A-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-949-016-150404
; Sequence 150404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150404
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150404
Query Match 5.4%; Score 33.8; DB 3; Length 601;
Best Local Similarity 52.5%; Pred. No. 0.57;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 63 TTCTTTGGTTAAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTAC 122
Db 131 TTTTTCGAGTGGGTCTATTTTAAATGTAATAAGCATAACATAAAATTTACTAT 190
Qy 123 GTCTCCCGCTCATAGTCTAGCACTCATTCGACATCGCAACATCAAGTCTGCTAGAC 182
Db 191 TTTTAAACAATTTTAAAGTGTACAGTAGCATTTACACATTTTACATCATTTGTGAGCTGTAC 250
Qy 183 TTCACTCTTCTCAGTCGAAGTT 203
Db 251 TACCATCACTCTAGAACTT 271
RESULT 2
US-09-949-016-15970
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

Db 18 KWKSHSYWYKWKYWKTYWRWRKCKCAWKKYKKTWTWWYWRVAMWGTYYKCKAMCRTK 77

```

416 111ATCAGCGCGGATTCACCTGCTGAGATATATGCAATATACAAATTCAGGGACATATCCGA 4/5
Db 78 TTKKCKCKGYNMMWYMGWRBSYNAMWTRTWTGYAYYRSMMYWMRYRCWKCKAYYRKTTCYS 137
Qy 476 CCGACCTCAACCCCTGCTGTGTCATCAGCAGCAAACTCTGCTATTGATTCGCGGATTTTA 535
Db 138 SKGWTWKKWKKAATTTWKKYTYWATRYWMMWMTWKWRASWYCWMMGKARKWSTWR 197
Qy 536 TGACATATGTCACGTCGGCGCAGCACTACTCACTTGTGCTCTCCATGGGTTTTCTTCGGGT 595
Db 198 KRSYSASARSARKCCYCSGWSGMSWYMWYMRWRGWTAGWAKAWRASOMMRKYAGKS 257
Qy 596 CAGATGAAACGACGTATGCT 615
Db 258 KTSYKSMWMCWTRSWKYCYT 277

RESULT 7
US-09-949-016-15440/c
; Sequence 15440, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15440
; LENGTH: 99304
; TYPE: DNA
; ORGANISM: Human

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; NAME/Ref: mabc_feature
; LOCATION: (1)...(99304)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15440

Query Match          5.2%; Score 32; DB 3; Length 99304;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 80; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 307 ACCGCAATGGTGGCGTTTGGGTTATCAACATCACATAAGAAATGACGGACTCCACTCCT 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41626 ACTGTTAACTCTGCTTTTCAGACACAGCAAGATACAAGAAACATAAGTATATTGTTG 41567

QY 367 ATGGAGGTCGTTGATGGCATAATTCATTGTCAGAACTTTAAACGGGAACGTTTATCAGCGG 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41566 GTGGAGGTTTTAGATGGAAGATTCGCTTTCTGAATACTACACTAAAAGGACTCAGAAAGG 41507

QY 427 GATTCCTACTGCTGAGATATATGCAATACAAATTCAGGGA 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41506 AATTATATCAAGAAACAAATATACTATAAATAGTGGA 41467

RESULT 8

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US-03-619-233A-10/C
; Sequence 18, Application US/09679299A
; Patent No. 6566135
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt

```

; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 6 EXPRESSION

; FILE REFERENCE: RTS-0187

; CURRENT APPLICATION NUMBER: US/09/679,299A

; CURRENT FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 164

; SEQ ID NO 18

; LENGTH: 17000

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-679-299A-18

Query Match 5.1%; Score 31.4; DB 3; Length 17000;

Best Local Similarity 51.0%; Pred. No. 17;

Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 318 TGGCTTTGGGTATCAACATCACCATAAGAAATGACGGATCCACTCTATGGAGTCTG 377

Db 16986 TGCTTTTCTTTTCCCATGACAGGCTAAAGAAATCCCTGAAACAGCGCGCTCTCTC 16927

Qy 378 TGATGGCATATTCATTTGCGAAGCTTAAACGGGAACGTTTATCAGCGGATCTACTGC 437

Db 16926 TGTTTGCATATGCAATGCAAGTAGAAGAACTCAATGAAAGAAATTAATCTTACAGTTTAAATGT 16867

Qy 438 TGATATATGCAAAATCAAAATCA 462

Db 16866 CGTCAGATTTTCCATTATGATTGA 16842

RESULT 9

US-09-949-016-15753/c

; Sequence 15753, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15753

; LENGTH: 236964

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(236964)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15753

Query Match 5.1%; Score 31.4; DB 3; Length 236964;

Best Local Similarity 50.3%; Pred. No. 58;

Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 328 GTTATCAATCACCATAAGAAATGACGGATCCACTCTATGGAGTCTGTGATGGCATA 387

Db 4225 GTTTATAACTTTGAATCATATAAGAAATTAATAATATGATGTGTCATTTCTTATC 4166

Qy 388 TTCCATTGCGAAGCTTAAACGGGAACGTTTATCAGCGGATCTTACTGCTGAGATATAT 447

Db 4165 TTTCATCTACAGTTTCAGAAACAGCAATTTTCTAAGCTTAGTTATACAGTGAAGTTAT 4106

Qy 448 GCAAAATCAAAATTCAGGAGCTATTCGACCCGAC 480

Db 4105 AACAACTCTAGTTCAACAAAATATTGATAGAC 4073

RESULT 10

US-09-221-017B-473

; Sequence 473, Application US/09221017B

; Patent No. 6444799

; GENERAL INFORMATION:

; APPLICANT: ROSS, Bruce C.

; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

; NUMBER OF SEQUENCES: 1120

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/221,017B

; FILING DATE: 23-DEC-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP1182

; FILING DATE: 31-DEC-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP1546

; FILING DATE: 30-JAN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP2911

; FILING DATE: 09-APR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/AU98/01023

; FILING DATE: 10-DEC-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: MORIKOV, Gladys H

; REGISTRATION NUMBER: 32,430

; REFERENCE/DOCKET NUMBER: 27340-20021.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-813-5600

; TELEFAX: 650-494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 473:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8439 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: UNKNOWN

; ORIGINAL SOURCE:

; ORGANISM: PORPHYROMONAS GINGIVALIS

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1...8439

US-09-221-017B-473

Query Match 5.0%; Score 31.2; DB 3; Length 8439;

Best Local Similarity 51.4%; Pred. No. 15;

Matches 72; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 255 AGTTAACTCCCTGCGACCAAGTTAAGAGTGTGGGTACGACGGGATAGGTGAAACCGCAAA 314

Db 5186 AGACAAATTCATTGAGGAATTTGGACGCGAGCGCTTAAATGGAACCGTGCACACGAAAT 5245

Qy 315 TGGTGGCTTTTGGGTTATCAATCACCATAAGAAATGACGGATCCACTCTCTATGGAGGT 374

Db 5246 GGGATTGTTGACAGTAATCAAAAAAATACTCCGGCTCGATGCCATCTGGCAAAAGC 5305

Qy 375 CGTTGATGGCATATTCCATT 394
Db 5306 CTATGCCGGCATTTGCTACT 5325

RESULT 11
US-09-710-279-1257/c
; Sequence 1257, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1257
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1257

Query Match 5.0%; Score 30.8; DB 3; Length 1995;
Best Local Similarity 52.3%; Pred. No. 10;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
|||||
Db 263 ATTGCGACGTGCTGATTATATCTCTCAAGAACTTAGTTTATCATCTCGTTTTTAAAGCG 204
|||||

Qy 210 TATCCCGTTTCACACATACGGAGGTAGGAGCTTGGAAATTAGATTACTCCCTGCA 269
Db 203 TAATCCTTATAAACTTACTTGGCGACATATACTAGCAAAATGGAAAGTGAATTGATTTT 144
|||||

Qy 270 GCAAGTTAAG 279
Db 143 GCGTATTTCAG 134
|||||

RESULT 12
US-09-134-001C-2645/c
; Sequence 2645, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2645
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2645

Query Match 5.0%; Score 30.8; DB 3; Length 2169;
Best Local Similarity 52.3%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
|||||

Db 437 ATTGCGACGTGCTGATTATATCTCAAGAACTTAGTTTATCATTCGTTTTTAAAGCG 378
Qy 210 TATCCCGTTTCACACATACGGAGGTAGGAGACTTGGAAATTAGATTACTCCCTGCA 269
|||||
Db 377 TAATCCTTATAAACTTACTTGGCGACATATACTAGCAAAATGGAAAGTGAATTGATTTT 318
|||||

Qy 270 GCAAGTTAAG 279
Db 317 GCGTATTTCAG 308
|||||

RESULT 13
US-09-710-279-3920/c
; Sequence 3920, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3920
; LENGTH: 3356
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3920

Query Match 5.0%; Score 30.8; DB 3; Length 3356;
Best Local Similarity 52.3%; Pred. No. 13;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
|||||
Db 666 ATTGCGACGTGCTGATTATATCTCTCAAGAACTTAGTTTATCATTCGTTTTTAAAGCG 607
|||||

Qy 210 TATCCCGTTTCACACATACGGAGGTAGGAGACTTGGAAATTAGATTACTCCCTGCA 269
Db 606 TAATCCTTATAAACTTACTTGGCGACATATACTAGCAAAATGGAAAGTGAATTGATTTT 547
|||||

Qy 270 GCAAGTTAAG 279
Db 546 GCGTATTTCAG 537
|||||

RESULT 14
US-09-539-333D-185
; Sequence 185, Application US/09539333D
; Patent No. 8476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Bessieux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 185
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-25917-115 : polymorphic base G or A
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1502..1520
; OTHER INFORMATION: 99-25917-115.mis1, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-25917-115.mis2,
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1595..1615
; OTHER INFORMATION: upstream amplification primer, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1115..1135
; OTHER INFORMATION: downstream amplification primer
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-25917-115 probe
US-09-539-333D-185

Query Match 4.9%; Score 30.6; DB 3; Length 3001;
Best Local Similarity 62.3%; Pred. No. 14;
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTCGTTTGGGTTATCAACATCACCAATGAAGAAATGACGGAT 358
Db 1276 TAAAGTAAACACAGATGTTCTTTTAGTCTGATCAAAATGAATAGGGACTATAGGTT 1335

Qy 359 CCACTCTATGAGGTC 375
Db 1336 CCACTCTTTTGAGCTC 1352

RESULT 15
US-09-949-016-151347/c
; Sequence 151347, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151347
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151347

Query Match 4.9%; Score 30.4; DB 3; Length 601;
Best Local Similarity 50.7%; Pred. No. 8.1;
Matches 73; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 395 TGCAGAACTTAAACGGGAAGCTTTATCAGCCGGATTCTACTGCTGAGATATATGCAATA 454
Db 145 TTCAGAGTAGCTCAGCGAGGAAGCAGTTGCAATTGTTACTTTGAAGATAAAGTCAACAG 86

Qy 455 CAAATTCAGGAGCTATTTCGACCGGACCTCAACCTGGTGTGTCATGACGACCAATCTCG 514
Db 85 GATCTACTCAGACAGGAGACCTTCGCACCTTTGCCAGAGTTTGACGAGGAGGATGATGG 26

Qy 515 TATTTGATATGCCGGATTTTATGA 538
Db 25 TGAGGTAAGTGAAGGACTCTGATGA 2

Search completed: April 12, 2006, 08:21:09
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GenCore version 5.1.7
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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 19587084
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES												
Result No.	Score	Query Match	Length	DB ID	Description							
1	621	100.0	744	9	US-10-784-592-18	Sequence 18, Appl						
2	35.2	5.7	580	9	US-10-487-901-4181	Sequence 4181, Ap						
3	35	5.6	2349	6	US-10-369-493-37301	Sequence 37301, A						
4	34.4	5.5	4818	7	US-10-437-963-69024	Sequence 69024, A						
5	34.2	5.5	1502	4	US-09-925-065A-429103	Sequence 724617,						
6	33.8	5.4	591	4	US-09-925-065A-867215	Sequence 867215,						
7	33.8	5.4	660	8	US-10-425-115-125681	Sequence 125681,						
8	33.8	5.4	729	7	US-10-425-114-6745	Sequence 6745, Ap						
9	33.8	5.4	860	7	US-10-425-114-6834	Sequence 6834, Ap						
10	33.8	5.4	935	8	US-10-425-115-154424	Sequence 154424,						
11	33.8	5.4	1240	4	US-09-925-065A-41609	Sequence 41609, A						
12	33.4	5.4	706	9	US-10-487-901-3702	Sequence 3702, Ap						
13	33.4	5.4	1048	7	US-10-767-701-11172	Sequence 11172, A						
14	33.2	5.3	534	4	US-09-925-065A-427028	Sequence 427028,						
15	32.8	5.3	641	4	US-09-925-065A-178736	Sequence 178736,						
16	32.6	5.2	566	4	US-09-925-065A-604703	Sequence 604703,						
17	32.6	5.2	566	4	US-09-925-065A-604704	Sequence 604704,						
18	32.6	5.2	2700	7	US-10-683-516-4	Sequence 4, Appl1						
19	32.4	5.2	611	4	US-09-925-065A-760902	Sequence 760902,						
20	32.4	5.2	813	7	US-10-282-122A-16587	Sequence 16587, A						
21	32.4	5.2	301477	7	US-10-322-281-456	Sequence 456, App						
22	32.2	5.2	598	4	US-09-925-065A-301137	Sequence 301137,						
23	32.2	5.2	123526	3	US-09-910-185-11	Sequence 11, Appl						

24	32	5.2	1470	7	US-10-437-963-89649	Sequence 89649, A
25	32	5.2	26147	10	US-11-097-143-14227	Sequence 14227, A
26	31.8	5.1	533	4	US-09-925-065A-413580	Sequence 413580,
27	31.8	5.1	534	6	US-10-264-049-1203	Sequence 1203, Ap
28	31.8	5.1	573	4	US-09-925-065A-429103	Sequence 429103,
29	31.8	5.1	615	4	US-09-925-065A-517010	Sequence 517010,
30	31.8	5.1	383432	9	US-10-737-082-34	Sequence 34, Appl
31	31.8	5.1	383432	9	US-10-765-790-34	Sequence 34, Appl
32	31.6	5.1	323	6	US-10-063-685-126	Sequence 126, App
33	31.6	5.1	704	9	US-10-487-901-6016	Sequence 6016, Ap
34	31.6	5.1	1007	9	US-10-487-901-4206	Sequence 4206, Ap
35	31.6	5.1	1394	4	US-09-925-065A-711186	Sequence 711186,
36	31.4	5.1	501	7	US-10-424-599-11847	Sequence 11847, A
37	31.4	5.1	540	4	US-09-925-065A-747461	Sequence 747461,
38	31.4	5.1	545	4	US-09-925-065A-746148	Sequence 746148,
39	31.4	5.1	567	5	US-10-027-632-139918	Sequence 139918,
40	31.4	5.1	567	6	US-10-027-632-139918	Sequence 139918,
41	31.4	5.1	611	4	US-09-925-065A-226317	Sequence 226317,
42	31.4	5.1	709	7	US-10-767-701-8345	Sequence 8345, Ap
43	31.4	5.1	735	5	US-10-184-644-88	Sequence 88, Appl
44	31.4	5.1	735	5	US-10-184-634-88	Sequence 88, Appl
45	31.4	5.1	1033	7	US-10-437-963-14402	Sequence 14402, A

ALIGNMENTS

RESULT 1
US-10-784-592-18
; Sequence 18, Application US/10784592
; Publication No. US20050147983A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Ostergaard, Peter
; APPLICANT: Lassen, Soren
; TITLE OF INVENTION: POLYPEPTIDES OF ALICYCLOBACILLUS SP.
; FILE REFERENCE: 10406.203-US
; CURRENT APPLICATION NUMBER: US/10/784,592
; CURRENT FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Alicyclobacillus sp.
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)..(744)
; OTHER INFORMATION: CDS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(123)
; OTHER INFORMATION: sig_peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (124)..(744)
; OTHER INFORMATION: mat_peptide
US-10-784-592-18

Query Match		100.0%;	Score 621;	DB 9;	Length 744;
Best Local Similarity		100.0%;	Pred. NO. 2.1e-201;		
Matches 621;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AACACGGTGTATATGATTTCGAGGAAACACACCGGGGAACGCATCAACGGTAAGCGCTACA	60		
Db	124	AACACGGTGTATATGATTTCGAGGAAACACACCGGGGAACGCATCAACGGTAAGCGCTACA	183		
Qy	61	ACTCTTTTGGTTAATTCGACGAATAGTTCACAGTAGCAAGCAAGCAAACTCGAGT	120		
Db	184	ACTCTTTTGGTTAATTCGACGAATAGTTCACAGTAGCAAGCAAGCAAACTCGAGT	243		
Qy	121	ACGTCCTCCGCTATAAGTCTACCACTTCATTGCAACATGGCGCAACATCAAGCTGCTACG	180		

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69732C.1
US-10-437-963-69024

Query Match 5.5%; Score 34.4; DB 7; Length 4818;
Best Local Similarity 50.0%; Pred. No. 6.2;
Matches 86; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 435 TGCTGAGATATATCAAAATACAAATTCAGGAGCTATTCGAGCCGACCTCAACCTCGTGT 494
DB 939 TACTGAATAGTACAGAGGAAAGGCGGCGAATATTAACCTGACCCAGATCTTGATGT 998
QY 495 GTCCATCAGACAAATCTCGTATTTGATATCCCGGATTTTATGACATATGTCACGTCGG 554
DB 999 TTACATGAGGCATATCATAGTGGGTGTCAGGAGCAAAATATCATCTGATTACGCTCT 1058
QY 555 GCAGCATTAATCACTTCCTCGCTCCATCGGTTTCTTCGGGTTCAGATGAAACG 606
DB 1059 CAAGATTCAGGACTTGACATTTGCGCTGACACCAATGTTTGGAAATGAATG 1110

RESULT 5

US-09-925-065A-724617/c
; Sequence 724617, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 724617

; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-724617

Query Match 5.5%; Score 34.2; DB 4; Length 1502;
Best Local Similarity 45.6%; Pred. No. 3.8;
Matches 120; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 197 CGAAGTTACATATATCCCGTTTCCACATACCGGAAGGTAGGACCTTGGAAATTAGAG 256
DB 783 CTAATGTAGGAGCATTTCTGGCATGCTCAAAGACCAGCAAGAGCGCTGTGTGGATAGAG 724
QY 257 TTAATCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGATAGGTAACCGCAATG 316
DB 723 TGAAGTGGATGGGTGTGGAAGGAAGTAGTATATGTTAAGAGATGTACAGGAGTC 664
QY 317 GTGCGTTTGGGTTATCAACATCACACCAATGACCGATCCACCTCTATGAGGTCG 376
DB 663 AGATAATTAGGCTTTGAGGCCACCATAGAAATTTTGGCTTTTCTTCAAGTTATATAG 604
QY 377 TTGATGCGATATTCATTTGAGCAACTTAACCGGGAACGTTTATCAGCGGATTTCTACTG 436
DB 603 AAGAAGAATATTCAAATTTTAAACCTTTTCTGTGTCATGAATTAATAAAGAATACATGA 544
QY 437 CTGAGATATATGCAATCAAT 459
DB 543 AAATGAAATGTACATCTCAATAT 521

RESULT 6

US-09-925-065A-867215
; Sequence 867215, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 867215

; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-867215

Query Match 5.4%; Score 33.8; DB 4; Length 591;
Best Local Similarity 52.5%; Pred. No. 3.1;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 63 TTCTTTGGTTAATTCGACGATAGTTCCACAGGTAGCAAGCAAGCAAACTCGAGTAC 122
DB 289 TTTTITTTTGGTGGGTCTATTTTAAATGTAATAGCATTAACATAAAATTTACTAT 348
QY 123 GTCTCCCGCTCATAAGTCTACGAACCTCATTCGCAACATCGCAACATCAAGCTGTACGAC 182
DB 349 TTAAACAATTTTAAAGGTACAGTAGCATTAACAACATTTACATCATTTGTGCAGCTGTAC 408
QY 183 TTCAATCTTCTCAGTCGAAT 203
DB 409 TACCATCCATCTCTAGAACTT 429

RESULT 7

US-10-425-115-125681
; Sequence 125681, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 125681
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46091C.1
US-10-425-115-125681

Query Match 5.4%; Score 33.8; DB 8; Length 660;
Best Local Similarity 52.5%; Pred. No. 3.3;

```
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 CTGGGCATATGACCGGAGTCAAGCCCGAGTGCCAAACGATGTTTAGGAATGGG 450
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 TTTCACGGGATCTCTCTGATATTACGTCGTCTGAGAGAATTACGTACGTGTCGCTCCTA 510
QY 581 TGGGTTTCTTCGGGTCCAGATG 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 TGAGTGTAGCCGACGTACG 531

RESULT 8
US-10-425-114-6745
; Sequence 6745, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6745
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700577561_FLI
US-10-425-114-6745

Query Match 5.4%; Score 33.8; DB 7; Length 729;
Best Local Similarity 52.5%; Pred. No. 3.5;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CTGGGCATATGACCGGAGTCAAGCCCGAGTGCCAAACGATGTTTAGGAATGGG 523
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 TTTCACGGGATCTCTCTGATATTACGTCGTCTGAGAGAATTACGTACGTGTCGCTCCTA 583
QY 581 TGGGTTTCTTCGGGTCCAGATG 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TGAGTGTAGCCGACGTACG 604

RESULT 9
US-10-425-114-6834
; Sequence 6834, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6834
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700579892_FLI
US-10-425-114-6834

Query Match 5.4%; Score 33.8; DB 7; Length 860;
Best Local Similarity 52.5%; Pred. No. 3.8;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 600 CTGGGCATATGACCGGAGTCAAGCCCGAGTGCCAAACGATGTTTAGGAATGGG 659
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 TTTCACGGGATCTCTCTGATATTACGTCGTCTGAGAGAATTACGTACGTGTCGCTCCTA 719
QY 581 TGGGTTTCTTCGGGTCCAGATG 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 720 TGAGTGTAGCCGACGTACG 740

RESULT 10
US-10-425-115-154424
; Sequence 154424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 154424
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_72415C.1
US-10-425-115-154424

Query Match 5.4%; Score 33.8; DB 8; Length 935;
Best Local Similarity 52.5%; Pred. No. 4;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 593 CTGGGCATATGACCGGAGTCAAGCCCGAGTGCCAAACGATGTTTAGGAATGGG 652
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 TTTCACGGGATCTCTCTGATATTACGTCGTCTGAGAGAATTACGTACGTGTCGCTCCTA 712
QY 581 TGGGTTTCTTCGGGTCCAGATG 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 713 TGAGTGTAGCCGACGTACG 733

RESULT 11
US-09-925-065A-41609
; Sequence 41609, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41609
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-41609

Query Match 5.4%; Score 33.8; DB 4; Length 1240;
Best Local Similarity 51.0%; Pred. No. 4.7;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 361 ACTCCTATGGAGGTCGTTGATGGCATATTCATTTGCGAAGACTTAAACGGGAACGTTTAT 420
Db 145 ACTCTTTTACCTCAGCATGCTACTGTTCTGATGACCAAGATAAAAACTGAACTTTAAA 204
Qy 421 CAGCGGATTTCTACTGCTGAGATATGCAATACAAATTCAGGAGCTATTCGACCGAC 480
Db 205 AATCTCTCTTCCACTGTGTGTATATATAAAAAAAATACTGGACCTTTATCACCAAA 264
Qy 481 CTCAACCTGTGTGTGTCATGACGACAAATCTCGTAT 517
Db 265 GTCAACAATCAGTGAAAGATGTGCATCAGGAAT 301

RESULT 12

US-10-487-901-3702/c
; Sequence 3702, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; NUMBER OF SEQ ID NOS: 2004-02-26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3702
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3702

Query Match 5.4%; Score 33.4; DB 9; Length 706;
Best Local Similarity 47.4%; Pred. No. 4.7;
Matches 100; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy

233 AGGTAGCAGACTTGGAAATTAGCTTAACCTCCCTGCAGCAAGTTTAAGAGTGTGGGTACG 292
Db 578 ATGAGGACAGCTTGATGATTTTGTTCATCCACCATCTTCATGTGAAGTGTATGATCCA 519
Qy 293 ACGGATAGGTGAAACCGCAAAATGGTGGTTTGGGTTATCAACATCACCAATAAGAAATG 352
Db 518 GGTGAGTAAATCCAGGCAACTCTTGTGAGTGGGAAATCAGAAATCACCAGGAAGCTGGG 459
Qy 353 ACGGATCCACTCCTATGAGGTCCTTGATGGCATATTCATTTGCAGAACTTAAACGGGA 412
Db 458 CACGATGTCTCTTTTACATAGGTGCGCTCGTGGTGCATGGAAGAACAAATAGTTA 399
Qy 413 ACGTTTATCAGCGGATTTCTACTGCTGAGAT 443
Db 398 ACATCAATCACCAGCTTTCTCCGGTGAGAT 368

RESULT 13

US-10-767-701-11172
; Sequence 11172, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11172
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUSI3127_1
US-10-767-701-11172

Query Match 5.4%; Score 33.4; DB 7; Length 1048;
Best Local Similarity 55.7%; Pred. No. 5.9;
Matches 64; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 434 CTGCTGAGATATATGCAAAATACAAATTCAGGAGCTATTCGACCGACTCTAACCTGGTG 493
Db 910 CTGCGATGTGAATGTGAATGAATCACCAGCAATCAAGCAAAAGTTTACAAAGCCAAGTG 969
Qy 494 TGTCATGACGACAAATCTCGTATTTGTATGATGCGGATTTTATGACATATGTCATCA 548
Db 970 TGTATGTTGAAATGAATCAAGTGTTCATATGCGGTAGTGTGACAAATGTTAA 1024

RESULT 14

US-09-925-065A-427028/c
; Sequence 427028, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09

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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427028
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-427028
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Query Match      5.3%; Score 33.2; DB 4; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

QY 253 AGAGTTAACTCCCTGCGAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAACCGCA 312
Db 191 ACATTTAACAGGCTGCAAGAAGTTGCTTCTCTCCCAATGGGGTAGGTCAGGACT 132
QY 313 AATGGTGGTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTCTATGGAG 372
Db 131 CACAGAGAGTCAGGGCTTTTCATCATTAACACAGAGTAAAGAGCCATTACCCCCCATGGTG 72
QY 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGGTGGCCATGT 56
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RESULT 15

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US-09-925-065A-178736/c
; Sequence 178736, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178736
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-178736
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Query Match      5.3%; Score 32.8; DB 4; Length 641;
Best Local Similarity 55.2%; Pred. No. 7.1;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 176 CTACGACTTCATCTTCTCAGTCGAAGTTACGATATATCCCGTTTCACACATACGGGAAGG 235
Db 618 CTTTGTCTTCATTTTAAATATAAATAAAGTATACCTTGTTCCTCCCTTTGCTTCTTGG 559
QY 236 TAGGAGACTTGGAAATTAGATTAACTCCCTGCGAGCAAGTTAAGAGTGTGGGTAC 291
Db 558 TATAGCGCTGTAAGCTTACATAAATTTCCCGAGCATTCAGTTTAAAGCTGTGGATAC 503
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Job time : 800 secs

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(without alignments)
3733.258 Million cell updates/sec
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Perfect score: 621
Sequence: 1 aaacggtgatgatgctg.....aaacgacgtatgctcttcg 621
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9281099 seqs, 2013915447 residues
Total number of hits satisfying chosen parameters: 18562198
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /SIDSS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDSS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDSS5/ptodata/2/pubpna/US05_NEW_PUB.seq:*
6: /SIDSS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
8: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
12: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
15: /SIDSS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query		Length	DB	ID	Description		
		Match	%						
c	1	34.2	5.5	1502	6	US-09-925-065A-724617	Sequence 724617,		
	2	33.8	5.4	591	6	US-09-925-065A-867215	Sequence 867215,		
	3	33.8	5.4	1240	6	US-09-925-065A-41609	Sequence 41609, A		
	4	33.8	5.4	1240	9	US-10-301-480-142847	Sequence 142847,		
	5	33.8	5.4	1240	10	US-10-301-480-756256	Sequence 756256,		
c	6	33.2	5.3	534	6	US-09-925-065A-427028	Sequence 427028,		
	7	33.2	5.3	534	10	US-10-301-480-490436	Sequence 490436,		
	8	33.2	5.3	534	10	US-10-301-480-1103845	Sequence 1103845,		
	9	32.8	5.3	641	6	US-09-925-065A-178736	Sequence 178736,		
	10	32.8	5.3	650	10	US-10-301-480-269706	Sequence 269706,		
c	11	32.8	5.3	650	10	US-10-301-480-883115	Sequence 883115,		
	12	32.6	5.2	566	6	US-09-925-065A-604703	Sequence 604703,		
	13	32.6	5.2	566	6	US-09-925-065A-604704	Sequence 604704,		
	14	32.4	5.2	611	6	US-09-925-065A-760902	Sequence 760902,		
	15	32.2	5.2	598	6	US-09-925-065A-301137	Sequence 301137,		
c	16	31.8	5.1	533	6	US-09-925-065A-413580	Sequence 413580,		
	17	31.8	5.1	551	10	US-10-301-480-479582	Sequence 479582,		
	18	31.8	5.1	551	10	US-10-301-480-1092991	Sequence 1092991,		

c	19	31.8	5.1	557	10	US-10-301-480-492045	Sequence 492045,
c	20	31.8	5.1	557	10	US-10-301-480-1105454	Sequence 1105454,
c	21	31.8	5.1	573	6	US-09-925-065A-429103	Sequence 429103,
c	22	31.8	5.1	615	6	US-09-925-065A-517010	Sequence 517010,
c	23	31.6	5.1	1394	6	US-09-925-065A-711186	Sequence 711186,
c	24	31.4	5.1	540	6	US-09-925-065A-747461	Sequence 747461,
c	25	31.4	5.1	545	6	US-09-925-065A-746148	Sequence 746148,
c	26	31.4	5.1	611	6	US-09-925-065A-226317	Sequence 226317,
c	27	31.4	5.1	1848	8	US-10-467-657-1219	Sequence 1219, Ap
c	28	31.2	5.0	505	10	US-10-301-480-471976	Sequence 471976,
c	29	31.2	5.0	505	10	US-10-301-480-1085385	Sequence 1085385,
c	30	31.2	5.0	524	6	US-09-925-065A-405101	Sequence 405101,
c	31	31.2	5.0	1173	8	US-10-517-939-27	Sequence 27, Appl
c	32	31.2	5.0	1715	11	US-11-096-568A-5015	Sequence 5015, App
c	33	31	5.0	23246	9	US-10-330-773-567	Sequence 567, App
c	34	30.8	5.0	505	10	US-10-301-480-1085384	Sequence 1085384,
c	35	30.8	5.0	524	6	US-09-925-065A-405100	Sequence 405100,
c	36	30.8	5.0	571	6	US-09-925-065A-488015	Sequence 488015,
c	37	30.8	5.0	641	6	US-09-925-065A-772763	Sequence 772763,
c	38	30.8	5.0	648	6	US-09-925-065A-768565	Sequence 768565,
c	39	30.8	5.0	846	6	US-09-925-065A-94388	Sequence 94388, A
c	40	30.8	5.0	846	9	US-10-301-480-195630	Sequence 195630,
c	41	30.8	5.0	846	10	US-10-301-480-809039	Sequence 809039,
c	42	30.8	5.0	1995	8	US-10-793-626-1257	Sequence 1257, Ap
c	43	30.8	5.0	3356	8	US-10-793-626-3920	Sequence 3920, Ap
c	44	30.6	4.9	507	6	US-09-925-065A-512361	Sequence 512361,
c	45	30.6	4.9	622	6	US-09-925-065A-733858	Sequence 733858,

ALIGNMENTS

RESULT 1
US-09-925-065A-724617/c
; Sequence 724617, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724617
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-724617

Query Match	5.5%;	Score 34.2;	DB 6;	Length 1502;
Best Local Similarity	45.6%;	Pred. No. 3.4;		
Matches 120;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;
Qy	197	CGAGTTACGATATATCCCGTTTCACATACCGGAGGTAGGAGCTTGGAATTAGAG	256	
Db	783	CTAATGTAGGAGCATTTCTTGGCATGCTCAAGACACGAAAGCCTGTGTGGATAGAG	724	
Qy	257	TTAACCTCCCTGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAAACCGCAATG	316	
Db	723	TGAAGTGGATGGTGTGAAAGGAAGTAGTATATATGTGGTAAAGAGTGAACAGGAGGTC	664	

Qy 317 GTGGTGGTTGGTTATCAACATCACCATAGAAATGACGATCCACTCTCTATGAGGTG 376
Db |||||
663 AGATAATTAGGGCTTTGAGGCCACCATAGAAATTTGGCTTTTCTTCAAGTTATAG 604
Qy 377 TTGATGGCATATTCATTTGAGAACTTAAACGGGAACGTTTATCAGCCGGAATCTACTG 436
Db |||||
603 AAGAAGAATATTCAAATTTTAAACCTTTCTGTGCATGAATTAATAAAGAATACATGA 544
Qy 437 CTGAGATATATGCAATACAAAT 459
Db |||||
543 AAATGAATGTACATCTCAATAT 521

RESULT 2

US-09-065A-867215
; Sequence 867215, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 867215
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-867215

Query Match 5.4%; Score 33.8; DB 6; Length 591;
Best Local Similarity 52.5%; Pred. No. 3.1;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 63 TTCTTTGGTTAAATTCGAGTAATGTCACAGGTAGCAAGCAAGCAAGCAAACTCGAGTAC 122
Db TTTTCTTTGGTGGTCTATTTTAAATGTAAGCAATACATATAAAATTTACTAT 348
Qy 123 GTCTCCGCTCATAGTCTACGAATCTTTCGAACATCGGCAACATCAAGCTGCTACGAC 182
Db TTTTAAACAATTTTAAAGTGTCAGTAGCATTAACAATTTACATATTGTGAGCTGTAC 408
Qy 183 TTCATCTTCTCAGTCGAAGTT 203
Db 409 TACCATCCNCTCTAGAACTT 429

RESULT 3

US-09-925-065A-41609
; Sequence 41609, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41609
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-41609

Query Match 5.4%; Score 33.8; DB 6; Length 1240;
Best Local Similarity 51.0%; Pred. No. 4.3;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
Qy 361 ACTCCTATGGAGGTGCTGTGATGGCATATTCATTTGCAGAACTTTAAACGGGAACGTTTAT 420
Db |||||
145 ACTCTTTTACTCTACGATGCTACTGTTTCTGATGACCAAGATATAAACTGAACCTTTAAA 204
Qy 421 CAGCCGGAATCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTTCCGACCGAC 480
Db |||||
205 AATCTCTCTTCCACCTGTGTATATATAAAAAAAATACTGACCTTTTATCACCAAA 264
Qy 481 CTCAACCTGCTGTGTCATGACGACCAAAATCTCGTAT 517
Db |||||
265 GTCAACAATCCAGTGAAGATGTGCATCAGGAAT 301

RESULT 4

US-10-301-480-142847
; Sequence 142847, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142847
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-142847

Query Match 5.4%; Score 33.8; DB 9; Length 1240;
Best Local Similarity 51.0%; Pred. No. 4.3;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
Qy 361 ACTCCTATGGAGGTGCTGTGATGGCATATTCATTTGCAGAACTTTAAACGGGAACGTTTAT 420
Db |||||
145 ACTCTTTTACTCTACGATGCTACTGTTTCTGATGACCAAGATATAAACTGAACCTTTAAA 204
Qy 421 CAGCCGGAATCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTTCCGACCGAC 480
Db |||||
205 AATCTCTCTTCCACCTGTGTATATATAAAAAAAATACTGACCTTTTATCACCAAA 264
Qy 481 CTCAACCTGCTGTGTCATGACGACCAAAATCTCGTAT 517
Db |||||
265 GTCAACAATCCAGTGAAGATGTGCATCAGGAAT 301

RESULT 5

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US-10-301-480-756256
; Sequence 756256, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 756256
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-756256

Query Match          5.4%; Score 33.8; DB 10; Length 1240;
Best Local Similarity 51.0%; Pred. No. 4.3;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 361 ACTCTATGGAGGTCGTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTTAT 420
Db 145 ACTCTTTTACCTCAGCATGCTACTGTTTCTGATGACCAAGATAAAACTGAACCTTTAAA 204
Qy 421 CAGCGGATTTCTACTGCTGAGATATATGCAATACAAATTCAGGAGCTATTCGACCGAC 480
Db 205 AATCTCTCTTCACTGTTGTATATATATAAAAAAATAACTGAGACCTTTTATCACCAAA 264
Qy 481 CTCAACCTGCTGTGTCATGACGACAAATCTCGTAT 517
Db 265 GTCAACAATCCAGTGAAGAAAGTGTCAATCAGGAAT 301

RESULT 6
US-09-925-065A-427028/c
; Sequence 427028, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 427028
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-427028

Query Match          5.3%; Score 33.2; DB 6; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

Qy 253 AGAGTTAACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATAGGTGAACCGCA 312
```

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Db 191 ACATTTAAACAGGCTGCAAGAAGTTGCTCTCTCCCAITGGGGTAGGTGAGACT 132
Qy 313 AATGGTGCCTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTTATGGAG 372
Db 131 CACAGAGAGTCAGGCTTTTTCATCATTTACACAGAGTAAAGAGCCATTTCACCCCATGGTG 72
Qy 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGTGGGCCATGT 56

RESULT 7
US-10-301-480-490436/c
; Sequence 490436, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 490436
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-490436

Query Match          5.3%; Score 33.2; DB 10; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

Qy 253 AGAGTTAACTCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGGATAGGTGAACCGCA 312
Db 191 ACATTTAAACAGGCTGCAAGAAGTTGCTCTCTCCCAITGGGGTAGGTGAGACT 132
Qy 313 AATGGTGCCTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTTATGGAG 372
Db 131 CACAGAGAGTCAGGCTTTTTCATCATTTACACAGAGTAAAGAGCCATTTCACCCCATGGTG 72
Qy 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGTGGGCCATGT 56

RESULT 8
US-10-301-480-1103845/c
; Sequence 1103845, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1103845
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapien
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 604703
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-604703

Query Match      5.2%; Score 32.6; DB 6; Length 566;
Best Local Similarity 55.9%; Pred. No. 7.5;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 151 TTGCAACATGCGCAACATCAAGCTGCTACGACTTCATCTTCTCAGTCGAAGTTACGATAT 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 TTGTTACATCAGCAACTAGGAACCTAATGCACATTCCTGTTTTCAGAGGGTCTTGAAG 149

Qy 211 ATCCCGTTTCACATACGGAAGGTAGGACCTTGGAAATAGAGTTAAC 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 TTCTGTTGAACACTTGCCAACTTGTGTAGTCTCGGTGTTTCATTTAAC 200

RESULT 13
US-09-925-065A-604704
; Sequence 604704, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 604704
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-604704

Query Match      5.2%; Score 32.6; DB 6; Length 566;
Best Local Similarity 55.9%; Pred. No. 7.5;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 151 TTGCAACATGCGCAACATCAAGCTGCTACGACTTCATCTTCTCAGTCGAAGTTACGATAT 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 TTGTTACATCAGCAACTAGGAACCTAATGCACATTCCTGTTTTCAGAGGGTCTTGAAG 149

Qy 211 ATCCCGTTTCACATACGGAAGGTAGGACCTTGGAAATAGAGTTAAC 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 TTCTGTTGAACACTTGCCAACTTGTGTAGTCTCGGTGTTTCATTTAAC 200

RESULT 14
US-09-925-065A-760902/c
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; Sequence 760902, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 760902
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-760902

Query Match      5.2%; Score 32.4; DB 6; Length 611;
Best Local Similarity 52.2%; Pred. No. 8.9;
Matches 72; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 30 ACCCGGAACGATCAACGCTAGCGCTACAACTTCTTTGGTTAATTCGAGATAGTTC 89
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 ACCCAAGACCTGTTACACTGTATATCTCTCTCTCCATGGGTTAATCCCCCAATTAGAGT 232

Qy 90 ACAGGTAGCAAGCAAGAGCAAACTCGAGTACGTCTCCGCTCATAGTCTACGAACTC 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 TTAGATAAGGAGCTAAGATTGCGATCTTGGCATCAGTCACTTACAGATCTGAAATGAAATC 172

Qy 150 ATTGCAACATCGCGCAACA 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 AGTGCCACATTCCTCTATA 154

RESULT 15
US-09-925-065A-301137
; Sequence 301137, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301137
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301137
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Query Match      5.2%; Score 32.2; DB 6; Length 598;
Best Local Similarity 49.7%; Pred. No. 10;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 160 GCGCAACATCAAGCTGCTAGGACTTCTCTCAGTCGAAGTTACGATATATCCCGTTT 219
Db 382 GGGACAGATGATGGTGTCTCTACTCAACTATGGCAGACGCGAGTGGGGCTAGTTAGGAAAG 441

Qy 220 CACACATACGGGAAGGTAGGAGACTTGGAAATTAGAGTTAACTCCCTGCAGCAAGTTAAG 279
Db 442 GGCACGTTCAAGAATGTACGACAATTGATATCAAGGGTTAGATAGAAAGAGGAGATAAAG 501

Qy 280 AGTGTGGGGTACGACGGGATAGGTGAACCGCAATGGTGGTTT 324
Db 502 ACGGGGCTGGTTTCTGGCATGAGTAACTGAGTAAATTGTGTGTT 546

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Search completed: April 12, 2006, 08:18:46
Job time : 672 secs